GenCore version 5.1.6 ight (c) 1993 - 2004 Compugen Ltd.	irch, using sw model	26, 2004, 15:44:15; Search time 42.75 Seconds (without alignments) 75:522 Million cell updates/sec	12-950-1 SSLF 9	5.0 , Gapext 0.5	seqs, 358729299 residues	atisfying chosen parameters: 2002273	000000000000000000000000000000000000000	n Match 0% n Match 100% g first 45 summaries	Jeneseq_23Sep04:* geneseqp1980s:* geneseqp200b:* geneseqp201b:* geneseqp201s:* geneseqp203as:* geneseqp203ss:*	number of results predicted by chance to have a n or equal to the score of the result being printed, analysis of the total score distribution.	SUMMARIES	DB ID Descript	3 AAY67860 Aay67860 2 AAY67860 Dav67840	5 ABB07160 ABB07160 7	5 AAM51004 Aam51004	5 AAMS1003 AamS1003 5 AAMS1002 AamS1002	3 AAY67851 Aay67851	5 ABB07161 Abb07161	5 AAM51005 Aam51005 5 AAM50908 Aam50908	5 AAM50899 Aam50899 5 ABP53540 Abp53540	2 AAW38323 AAW38323 5 ABB07159 Abb07159	5 AAM51001 6 ARR84631 Abb84631	7 ADF09190 Adf09190	9 8 ADJ98875 Adj98875 7 6 ABB4634 Abb84634	7 ADF09193 AAY67859 3 AAY67855 AAY67855	9 3 AAY67856 Aay67856 S. aureus 9 5 AAMS0903 Aam50903 AgrD-auto
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26	27	28	29	30	31	32	33	34	ı,			88		40	41	4	. 4 . 6	4 4	45

ALIGNMENTS

Staphylococcus aureus infection; AgrD; agr response; treatment; virulence factor. Staphylococcus aureus AgrDII derived peptide sequence. Ji G, Beavis R; Muir TW, Mayville P, Novick RP, AAY67860 standard; peptide; 9 AA. 99WO-US014562. 98US-00103438. (UYNQ) UNIV ROCKEFELLER. (UYNY) UNIV NEW YORK STATE. 25-APR-2000 (first entry) Staphylococcus aureus. WPI; 2000-147202/13. WO9967286-A2. 24-JUN-1999; 24-JUN-1998; 29-DEC-1999. AAY67860; RESULT 1 AAY67860

New cyclic peptides for treating infections with Staphylococcus aureus. Example; Page 22; 37pp; English.

This sequence represents the Staphylococcus aureus AgrDII derived peptide. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus

Sequence 9 AA;

97.4%; Score 38; DB 3; Length 9; 88.9%; Pred. No. 1.7e+06; Query Match Best Local Similarity

Matches

ð ġ RESULT 2

AAY67859

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The invention relates to the use of autoinducer-2 (AI-2) agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis. Synergistic antibiotic compositions comprising inhibitors of the quorum-sensing pathway of a microorganism are also provided. Methods using such AI-2 analogues are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treating pathogen-associated disease states. The compounds and antibiotic compositions can be used to inhibit bacterial cell growth and/or biofilm formations can medical device, particularly for promoting growth of skin graft replacements used in the treatment of burns and ulcers. They may also be used to aid wound repair, and to inhibit bacterial cell growth and biofilm formation in or on products or devices used for personal hygiene. The present sequence represents a inhibitor of peptide-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "note linked to residue 9 to form cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                        Use of autoinducer-2 agonists or antagonists for regulating activity cautoinducer-2 receptor, regulating bacterial growth and pathogenesis, also antibiotic compositions.
       vulnerary, pheromone, agr system; accessory gene regulator; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic; antibacterial; infection; therapy; cyclic.
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                                                                                                                                                                                                                                                                                                                    Shokat K,
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Pred. No. 1.7e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 33; 134pp; English.
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                                                                                                                                                                                                                                      (UYPR-) UNIV PRINCETON.
(QUOR-) QUOREX PHARM INC.
(UYTE-) UNIV TECHNOLOGIES INT INC.
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07-DEC-2000; 2000US-0254398P.
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8; Conservative
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                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-075235/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9 AA;
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Modified-site
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                                        Synthetic
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents the Staphylococcus aureus AgrDII derived peptide. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New cyclic peptides for treating infections with Staphylococcus aureus.
     Gaps
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                                                                                                                                                                                                                                                                                                          Staphylococcus aureus infection; treatment; AgrD; agr response;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide-mediated quorum sensing inhibitor peptide cyclo-XII.
   1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 9;
                                                                                                                                                                                                                                                                         Staphylococcus aureus AgrDII derived peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beavis R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.4%; Score 38; DB 3; I
88.9%; Pred. No. 1.7e+06;
.ive 0; Mismatches 1;
 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novick RP,
                                                                                                                                                              AAY67859 standard; peptide; 9 AA.
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(UYNY ) UNIV NEW YORK STATE.
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Best Local Similarity 88.30,
8; Conservative
                                                                                                                                                                                                                                    (first entry)
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muir TW, Mayville P,
                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus,
                                  GVNAXSSLF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-147202/13.
                                                                   GVNASSSLF
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                                                                                                                                                                                                                                                                                                                             virulence factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JUN-1999;
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                                                                                                                                                                                                 AAY67859;
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Gaps

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1; Indels Length 9;

Modified-site

Autoinducer-2; AI-2; antibiotic; antibacterial; dermatological;

RESULT 3
ABB07160
ID ABB0
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AC ABB0
XX
DT 13-M
XX
XX
XX
KW AUCC

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Surette MG;

Stein J,

therapy; lactone; cyclic.

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The present sequence is that of a protected peptide used in an example of the preparation of novel synthetic cyclic peptides of the invention (see AAMS0899-906). The peptide corresponds to the Staphylococcus aureus acreain using an Fmoc N-alpha protection strategy. Howas synthesised on a Wang-resin using an Fmoc N-alpha protection strategy. Following thin assembly, the peptide was cleaved from the support and the Ser-5 cresidue deprotected by treatment with a trifluoroacetic acid:anisole:water mixture (90:5:5) for 4 hr. The partially protected peptide-alpha carboxylates were then dissolved in DMF and treated with complete after 2 hr. The remaining protecting groups were then removed by treatment with HF and the peptide purified by HPLC. The cyclization was complete of inhibiting the agr response of Staphylococcus aureus. The thololactone structure within native AgrD peptides is required for activation of this response. Replacement of the thiol ester component of the cyclic ring structure within alactone (as in the present case) or a lactam can desiroy agr response activating activity while preserving and enhancing inhibitory activity. The cyclic peptides are useful for chall interference, especially for the treatment of S. aureus
                                                                                               /note= "note linked to residue 5 to form cyclic peptide"
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                                                                                                                                                                                                                                                                                                                                                                               Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38; DB 5; Length 9;
Pred. No. 1.7e+06;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                   Beavis R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Col 14; 18pp; English.
                                                                                                                                                                                                                                                                                                                     Muir TW, Mayville P, Novick RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM51004 standard; peptide; 9 AA.
/note= "Ser(tBu)"
                                 note= "Ser(Bzl)"
                                                                 note= "Ser(Bzl)"
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(UYNY ) UNIV NEW YORK STATE.
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(first entry)
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Best Local Similarity 89..
8, Conservative
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                                                                                   Misc-difference
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08-MAY-2002
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The present sequence is that of a novel synthetic AgrD2 lactone cyclic peptide in which residue 5 of the peptide is linked to residue 9 via a lactone bond. The peptide is derived from an AgrD2 peptide of staphylococcus aurents group II. AgrD2 is a secreted agr-encoded peptide, staphylococcus aurents group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aurens. The biological activity of the synthetic peptide was assayed using cultured S. aurens strains containing a beta-lactamase reporter gene fused to the agr promoter. This allowed activation or inhibition of the agr response of group IS. aurens strains without activating the agr response in group I, II or III strains. The invention cultivating the agr response in group I, II or III strains. The invention provides claimed cyclic peptides (see AAN50899-906 and AAN50999) and continued for provides for preparing them, especially peptides are useful for bacterial interference, especially for the treatment of S. aurens infection.
                                                                                                        note= "note linked to residue 9 to form cyclic peptide"
                                                                                                                                       /note= "note linked to residue 5 to form cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in
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88.9%; Pred. No. 1.7e+06;
tive 0; Mismatches 1;
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                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AgrD2 linear free acid peptide.
                                                                                                                                                                                                                                                                          98US-0090402P.
                                                                                                                                                                                                                                           99US-00339511.
                                                                                                                                                                                                                                                                                                        (UYRQ ) UNIV ROCKEFELLER.
(UYNY ) UNIV NEW YORK STATE.
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                                Staphylococcus aureus.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-170774/22.
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les 8; Conserv
                                                                                                                         Misc-difference 9
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AAM51003
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of a novel synthetic AgrD2 linear free acid peptide. The peptide is derived from the cyclic AgrD2 peptide of Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured. S. aureus strains containing a beta-lactamase reporter gene fused to the synthetic peptide was assayed using cultured. S. aureus strains containing a beta-lactamase reporter gene fused to the synthetic peptide was unable to either cyclic peptide (see AAMS1001), the present peptide was unable to either at uM concentrations. The invention provides laimed cyclic peptides (see AAMS10899-906 and AAMS0899) and methods for preparing them. The cyclic peptides are useful for beaterial interference, especially for the
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88.9%; Pred. No. 1.7e+06;
iive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                      Novick RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment of S. aureus infection
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(UYNY ) UNIV NEW YORK STATE.
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Matches 8; Conservative
             Staphylococcus aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel synthetic,
interference and
subject.
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at uM concentrations. The invention provides claimed cyclic peptides (see AMS0899-906 and AAMS0899) and methods for preparing them. The cyclic peptides are useful for bacterial interference, especially for the treatment of S. aureus infection
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                                                                                                                                                                                                                                                                                                                                                                           Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in a
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                                                                                                                                                                                                                                                                  Beavis R,
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                                                    99US-00339511
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(UYNY ) UNIV NEW YORK STATE.
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Matches 8; Conserv
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                                                    24-JUN-1999;
                                                                                                               24-JUN-1998;
08-JAN-2002
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                                                                                                                                              This sequence represents a cyclic peptide derived from the Staphylococcus aureus AgrD peptide. The invention relates to AgrD derived peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that extivates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus
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                                                                                             New cyclic peptides for treating infections with Staphylococcus aureus.
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                                                                                                                                                                                                                                                                                                  Score 37; DB 3; Length 9; Pred. No. 1.7e+06; 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                         94.9%; Scur-
100.0%; Pre-
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                                                Novick RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY67861 standard; peptide; 9 AA.
                                                                                                                        Claim 9; Page 26; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unknown
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(UYNY ) UNIV NEW YORK STATE.
            (UYNQ ) UNIV ROCKEFELLER.
(UYNY ) UNIV NEW YORK STATE.
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                                                                                                                                                                                                                                                                                                                                9; Conservative
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                                                Mayville P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus.
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                                                                        WPI; 2000-147202/13.
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Best Local Similarity
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                                                Muir TW,
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composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of staphylococcus aureus. An AgrD peptide is produced by S. aureus that extivates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus
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                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Autoinducer-2; AI-2; antibiotic; antibacterial; dermatological; vulnerary; pheromone; agr system; accessory gene regulator; cyclic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide-mediated quorum sensing inhibitor peptide cyclo-XIII.
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                                                                                                                                                                                                                   Indels
                                                                                                                                                                                  Length
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                                                                                                                                                                                Score 37; DB 3; Le
Pred. No. 1.7e+06;
0; Mismatches 0;
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UNIV TECHNOLOGIES INT INC.
                                                                                                                                                                       94.9%; Scc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                    ABB07161 standard; peptide; 9 AA.
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2000US-0254398P.
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                                                                                                                                                                                                                                                                                          GVNAXSSLF 9
                                                                                                                                                               Query Match
Best Local Similarity
9; Conserv?
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                                                                                                                                                                                                                                                         1 GVNAXSSLF
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                                                                                                                                                Sequence 9 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                         ABB07161;
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us-10-032-950-1.rag

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Synthetic.
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                                                              Query Match
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                                                                                                                                                                  AAM50908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of a novel synthetic AgrD2 lactam cyclic peptide in which residue 5 of the peptide is linked to residue 9 via a lactam bond. The peptide is derived from an AgrD2 peptide of Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agr promoter. This allowed activation or inhibition of the agr response to be monitored spectrophotometrically. The AgrD3 lactam peptide inhibited the agr response in group I S. aureus strains and did not provides claimed cyclic peptides (see AAMS0899-906 and AAMS0999) and methods for preparing them, especially where the cyclic bond is a lactam
                                                                                                                                                                                                                                                                                                                               'note= "note linked to residue 9 to form cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                      /note= "note linked to residue 5 to form cyclic peptide"
                                                                                                                                                                                                                                               AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in
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                                                             0; Indels
                                        Length 9;
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                                        DB 5; Le
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                                       94.9%; Score 37; DB 100.0%; Pred. No. 1.7 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                    'note= "any amino acid"
                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novick RP,
                                                                                                                                                      AAMS1005 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0090402P,
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                                                                                                                                                                                                                           AgrD2 lactam cyclic peptide.
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(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                        (first entry)
                                      Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                              (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muir TW, Mayville P,
                                                                                                                                                                                                                                                                             Staphylococcus aureus
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                                                                                             GVNAXSSLF
                                                                               1 GVNAXSSLF
                                                                                                                                                                                                                                                                                                                     Misc-difference
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                                                                                                                                                                                                                                                         therapy; cyclic.
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  quorum sensing
                    Sequence 9 AA;
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08-MAY-2002
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                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                          AAM51005;
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AAM51005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "note linked to residue 5 to form cyclic peptide"
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                                                                                                                                                                                                                                   Gaps
or lactone bond. The cyclic peptides are useful for bacterial interference, especially for the treatment of S. aureus infection. (Updated on 07-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic; antibacterial; infection; therapy; cyclic.
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                                                                                                                                                                         94.9%; Score 37; DB 5; Length 9; 100.0%; Pred. No. 1.7e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protected peptide used in cyclic peptide production.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM50908 standard; peptide; 9 AA.
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(UYNY ) UNIV NEW YORK STATE.
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                                                                                                                                                                                                     Best Local Similarity 100.
Matches 9, Conservative
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                                                                                                                                                                                                                                                                                        1 GVNAXSSLF
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                                                                                                                 Sequence 9 AA;
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Modified-site
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partially protected peptide-alpha carboxylates were then dissolved in DWF and treated with PyBOP. Cyclization was complete after 2 hr. The remaining protecting groups were removed by treatment with HF and the peptide purified by HPLC. The cyclic peptide is capable of inhibiting the agr response of Staphylococcus aureus. The thiololactone structure within native AgrD peptides is required for activation of this response. Replacement of the thiol ester component of the cyclic ring structure with a lactam (as in the present case) or a lactone can destroy agr activity while preserving and enhancing inhibitory activity. The cyclic peptides are useful for bacterial interference, especially for the treatment of S. aureus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of a novel synthetic cyclic peptide of the invention that is capable of inhibiting the agr response of Staphylococcus aureus. It is an AgrD-autoinducing peptide, where AgrD is a secreted agr-encoded peptide and where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. Preferred peptides may have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "note linked to residue 9 to form cyclic peptide"
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                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                    Length 9;
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100.0%; Pred. No. 1.7e+06;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                    AAM50899 standard; peptide; 9 AA.
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(UYNY ) UNIV NEW YORK STATE.
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Best Local Similarity
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the sequence NH2-X(n)-Z-X(y)-COOH, with a cyclic bond between the Z residue and COOH other than a thioester bond, where X is an amino acid, an amino acid analogue, a peptidominetic or non-amide isostere, Z is a synthetic or a biosynthetic amino acid, n is 0-10 and y is 1-10. The cyclic bond is especially a lactam or lactone bond. The thiololactone cyclic bond is especially a lactam or lactone bond. The thiololactone at response. Elimination of the thiol ester component of the cyclic ring structure can destroy agr response activating activity while preserving cand enhancing inhibitory activity. A claimed method of preparing a cyclic peptide involves: assembling a linear peptide chain on to a solid phase resin support; deprotecting the resulting protected assembled peptide; treating the deprotected peptide with neutral buffer for a time sufficient to form the cyclic peptide and cleave the peptide from the support; and recovering the cyclic peptide. The peptide is useful for becterial interference, especially for the treatment of S. aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP53540 to ABP53547 represent cyclic peptides (I) from the present invention. The present invention also describes a method for treating
                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP53540 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                      Local Similarity 100.
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MAYVILLE F
NOVICK R F
BEAVIS R.
JI G.
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24-JUN-1999;
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(MAYV/) N
(NOVI/) N
(BEAV/) I
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcription inhibitory peptide; inhibition; antibiotic; abscesses; endocarditis; pneumonia; osteomyelitis; virulence factor; agr regulator; agr-rnaIII gene; colonisation.
Staphylococcus aureus infection comprising the administration of a composition comprising (I). (I) has ancibacterial activity, and can be used as an agr gene response inhibitor. The peptides are useful for treating S. aureus infections
                                                                                                                                                       Gaps
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                                                                                                                   94.9%; Score 37; DB 5; Length 9; 100.0%; Pred. No. 1.7e+06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                           Transcription inhibitory peptide 3.
                                                                                                                                                                                                                                                                                                          AAW38323 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                 Query Match
Best Local Similarity 100.
Matches 9; Conservative
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Misc-difference
                                                                                    Sequence 9 AA;
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Sequence 9 AA;

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   Score 36; DB 2; Length 9;
Pred. No. 1.7e+06;
0; Mismatches 1; Indels
                                                                                                                      Search completed: October 26, 2004, 15:59:38 Job time: 43.75 secs
92.3%; Scool 88.9%; Pred
         Query Match 92.3
Best Local Similarity 88.9
Matches 8; Conservative
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October 26, 2004, 15:54:00 ; Search time 31.5 Seconds (without alignments) 92.502 Million cell updates/sec
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| cgn2_6/ptodate/2/pubpaa/PCT_NEW_PUB.pep:*
| cgn2_6/ptodate/2/pubpaa/PCT_NEW_PUB.pep:*
| cgn2_6/ptodate/2/pubpaa/PCT_NEW_PUB.pep:*
| cgn2_6/ptodate/2/pubpaa/NGO_NEW_PUB.pep:*
| cgn2_6/ptodate/2/pubpaa/NGO_NEW_PUB.pep:*
| cgn2_6/ptodate/2/pubpaa/NGO_NEW_PUB.pep:*
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| cgn2_6/ptodate/2/pubpaa/NGOB_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004. Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1364641 segs, 323758627 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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39
1 GVNAXSSLF 9
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                                                                                                                                                                                                                                                          Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

; ; ; ;	1, Appli	3, Appli	6, Appli	5, Appli	6, Appli	2, Appli	7, Appli	4, Appli	189388,	227, App	130, App	131, App	6225, Ap
Description	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence
ΔΙ	US-10-032-950-1	US-10-201-444-3	US-10-201-444-6	US-10-032-950-5	US-10-032-950-6	US-10-032-950-2	US-10-032-950-7	US-10-032-950-4	US-10-437-963-18938B	US-10-108-605-227	US-10-004-378A-130	US-10-004-378A-131	US-10-369-493-6225
DB	13	14	14	13	13	13	13	13	16	13	14	14	14
% Query Watch Length DB	6	σ	47	σ	σ	σ	σ	σ	313	465	465	465	633
% Query Match	94.9	92.3	92.3	87.2	87.2	84.6	82.1	79.5	79.5	76.9	76.9	76.9	76.9
Score	37	36	36	34	34	33	32	31	31	30	30	30	30
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53	74.4	9	15	-	Sequence 260806,
29	74.4	81		1	Seguence 276931,
29	74.4	93		į	Sequence 205071,
29	74.4	167		į	Sequence 171012,
29	74.4	271		Ξ	Seguence 72245, A
53	74.4	294		Ţ	Sequence 40441, A
53	74.4	311		1	Seguence 1603, Ap
59	<#	317		Ξ	Sequence 48025, A
20	5#	332		Ξ	Sequence 46, Appl
29	*#	382		œ	Seguence 10385, A
29	511	382		Ä	Sequence 56166, A
29	7	382	15	Ä	Sequence 56741, A
0	ぜ	382	13	7	Sequence 60169, A
5	ਾਵਾ	382	15	Ä	Seguence 75336, A
20	ď	382	15	ä	Sequence 75407, A
29	4	411	16	į	Seguence 58, Appl
29	ぜ	416	14	Ξ	Sequence 26, Appl
29	4	416	14	7	Sequence 26, Appl
29	4	416	14	d	Sequence 26, Appl
29	ব্দ	416	14	5	Sequence 26, Appl
29	4	490	14	-	Sequence 3, Appli
29	ಶ್	490	14	-	Sequence 2, Appli
29	74.4	583	16	į	Seguence 168044,
29	4	605	14	-	Sequence 110, App
29	4	618	15	5	Seguence 78248, A
29	4	653	16	į	a)
29	4	747	σ	6-60-	edneuce
29	4	747	σ	9-9	equence 9,
29	4	747	o	-09-978-697-4	459
29	4	747	σ	-09-978-192A-4	459

RESULT 1 US-10-032-950-1 US-10-032-950-1 Sequence 1, Application US/10032950 Publication No. US2020007745341 GENERAL INFORMATION: APPLICANT: Maryille, Particia APPLICANT: Maryille, Particia APPLICANT: Maryille, Particia APPLICANT: Mayorille, Particia APPLICANT: Mayorille, Particia APPLICANT: Mayorille, Particia APPLICANT: Mayorille, Particia APPLICANT: No. US20200077453A11ck, Richard P. APPLICANT: No. US20200077453A11ck, Richard P. TILLE OF INVENTION: INTERPRENCE FILE REFERENCE: 600-1-231N CURRENT APPLICATION NUMBER: US/10/032,950 CURRENT FILING DATE: 200-12-27 PRIOR FILING DATE: 1998-06-24 NUMBER OF SEQ ID NOS: 8 SOFTWARE: Patentin Ver. 2.0 SOFTWARE: Patentin Ver. 2.0 SOFTWARE: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Peptide NAME/KEY: VARIANT LUCCATION: (5) COTHER INFORMATION: As a represents any amino acid at this position. US-10-032-950-1

ALIGNMENTS

1 GVNAXSSLF 9

8

Query Match

94.9%; Score 37; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels

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Gaps

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/10032950;
Publication No. US20020077453A1
GENERAL INFORMATION:
APPLICANT: Muir. TO:
APPLICANT: Moi. US20020077453A1ick, Richard P.
APPLICANT: No. US20020077453Aick, Richard P.
APPLICANT: No. US20020077453Aick, Richard P.
APPLICANT: Di, Guangyong
ITILE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
ITILE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
ITILE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
CURRENT PELLON NUMBER: US/10/032,950
CURRENT FILING DATE: 2001-12-27
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Var. 2.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Synthetic CTHER INFORMATION: peptide
| NAME/KEY: VARIANT | LOCATION: (5) | OTHER INFORMATION: Xaa represents any amino acid at this position. US-10-032-950-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
GRGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
NAME/KEY: VARIANT
LOCATION: (5)
OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-6
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Pred. No. 1.2e+06;
1; Mismatches 0; Indels
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TITLE OF INVENTION: INTERFERENCE
FILE REPERSIVE: 600-1-231N
CURRENT APPLICATION NUMBER: US/10/032,950
CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.9%;
                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 86...
8; Conservative
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US-10-032-950-6
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US-10-032-950-2
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VS-10-201-444-6

Sequence 6, Application US/10201444

Publication No. US2030078378A1

GENERAL INFORMATION:

APPLICANT: New York University Medical Center

APPLICANT: New York University Medical Center

TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE PACTORS IN S. AUREUS

FILE REFERENCE: 63753/7

CURRENT APPLICATION NUMBER: US/10/201,444

CURRENT PILING DATE: 1997-05-22

PRIOR FILING DATE: 1997-05-22

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin version 3.0

SEQ ID NO 6

LENGTH: 47
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                                                                                                                  USS-10-201-444-3
; Sequence 3. Application US/10201444
; Publication No. US20030078378A1
; Publication No. US20030078378A1
; GENERAL INFORMATION:
    APPLICANT: New York University Medical Center
; TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
; FILE REFERENCE: 63753/7
    CURRENT FILING DATE: 2002-07-23
; FILE REPLICATION NUMBER: US/10/201,444
; CHRENT FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NOS: 8
; SEQ ID NOS: 8
; SEQ ID NO 3
; LENGTH: 9
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| Publication No. US20020077453A1
| GENERAL INFORMATION: APPLICANT: Maryille, Patricia APPLICANT: No. US20020077453A1ick, Richard P. APPLICANT: No. US20020077453A1ick, Richard P. APPLICANT: Beavis. Ronald APPLICANT: Ji, Guangyong APPLICANT: ST. USANTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL ITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 92.3%; Score 36; DB 14; Length 9; Best Local Similarity 88.9%; Pred. No. 1.2e+06; Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-201-444-3
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1 GVNAXSSLF
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US-10-032-950-5
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GENERAL INFORMATION

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TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Oryza sativa
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APPLICANT: Muir, Tom
APPLICANT: Mayville, Patricia
APPLICANT: Mayville, Patricia
APPLICANT: Mayville, Patricia
APPLICANT: Mayville, Ronald
APPLICANT: Beavis, Ronald
APPLICANT: Boxis, Ronald
APPLICANT: Ji, Gunnayong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: UNTERPERENCE
FILE REFRENCE: 600-1-231N
CURRENT APPLICATION NUMBER: 60/090,402
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MAIT, Tom
APPLICANT: MAYOILLE, Patricia
APPLICANT: MAYOILLE, Patricia
APPLICANT: No. US200007453Alick, Richard P.
APPLICANT: Beavis, Ronald
APPLICANT: Beavis, Ronald
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: NOVER STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: NOVER: US/10/032,950
CURRENT APPLICATION NUMBER: 60/090,402
PRIOR PLILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOCATION: (5)
COTHER INFORMATION: Xaa represents any amino acid at this position. US-10-032-950-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
NAME/KEY: VARIANT
LOCATION: (5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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84.6%; Score 33; DB 13; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels
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Publication No. US20020077453A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 88.9
Matches 8; Conservative
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LENGTH: 9
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Sequence 189388

| Sequence 189388 | Application US/10437963 |
| Publication No. US2004012334341 |
| Publication No. US2004012334341 |
| GENERAL INFORMATION: |
| APPLICANT: La Rosa, Thomas J. |
| APPLICANT: Zhou, Yihua |
| APPLICANT: Zhou, Yihua |
| APPLICANT: Zhou, Yongwei |
| APPLICANT: Boukharov, Andrey A. |
| APPLICANT: Barbazuk, Brad |
| APPLICANT: Branch |
| APPLICANT: Li, Ping |
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement |
| FILE REFERENCE: 38-21 (53221) B |
| CURRENT APPLICATION NUMBER: US/10/437,963 |
| CURRENT FILING DATE: 2003-05-14 |
| NUMBER OF SEQ ID NOS: 204966 |
| SEQ ID NO 189388 |
| LENGTH: 313
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Sequence 4, Application US/10032950;
Publication No. US20020077453A1;
GENERAL INFORMATION:
APPLICANT: Muir, Tom
APPLICANT: Mayville, Patricia
APPLICANT: Mayville, Patricia
APPLICANT: No. US20020077453A1ick, Richard P.
APPLICANT: Deavis, Ronald
APPLICANT: Beavis, Ronald
APPLICANT: Beavis, Ronald
APPLICANT: Beavis, Ronald
APPLICANT: Beavis, Ronald
APPLICANT: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
FILE REFREENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/10/032,950
CURRENT FILING DATE: 1998-06-24
NUMBER: OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 4
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Xaa represents any amino acid at this position US-10-032-950-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 79.5%; Score 31; DB 13; Length 9; Best Local Similarity 100.0%; Pred. No. 1.2e+06; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT4530_85902C.1.pep
US-10-437-963-189388
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OTHER INFORMATION: unsure at all Xaa locations
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APPLICANT: Stone, David J
APPLICANT: Ellerman, Karen
APPLICANT: Ellerman, Karen
APPLICANT: Gangolli, Baha A
ITILE OF INVENTION: Methods of Using the Same
ITILE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 21402-179
CURRENT APPLICATION NUMBER: US/10/004,378A
CURRENT APPLICATION NUMBER: 60/242,882
FRIOR APPLICATION NUMBER: 60/242,765
FRIOR APPLICATION NUMBER: 60/242,765
FRIOR APPLICATION NUMBER: 60/242,765
FRIOR APPLICATION NUMBER: 60/242,765
FRIOR APPLICATION NUMBER: 60/242,768
FRIOR APPLICATION NUMBER: 60/242,768
FRIOR APPLICATION NUMBER: 60/242,768
FRIOR APPLICATION NUMBER: 60/242,768
FRIOR APPLICATION NUMBER: 60/243,622
FRIOR APPLICATION NUMBER: 60/243,622
FRIOR APPLICATION NUMBER: 60/243,622
FRIOR APPLICATION NUMBER: 60/243,622
FRIOR APPLICATION NUMBER: 60/243,591
FRIOR FILING DATE: 2000-10-26
FRIOR APPLICATION NUMBER: 60/243,591
FRIOR FILING DATE: 2001-0-27
FRIOR APPLICATION NUMBER: 60/243,591
FRIOR APPLICAT
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66.7%; Pred. No. 2.6e+02;
ive 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Drosophila melanogaster
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Shinkets, Richard A
Guo, Xiaojia Sasha
Casman, Stacie J
Burgess, Catherine E
Malyankar, Uriel M
Tchernev, Velizar T
Vernet, Corrine A
Spytek, Kimberly A
Agee, Michele
Rastelli, Luca
Shenoy, Suresh G
Grosse, William M
Alsobrook II, John P
Lepley, Denise M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Li, Li
APPLICANT: Furtak, Kazarzyna
APPLICANT: Ferna, Manda
APPLICANT: Perna, Manda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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APPLICANT:
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Sequence 227, Application US/10108605
Publication No. US20020160934A1
GENERAL INFORMATION:
Fublication No. US20020160934A1
GENERAL INFORMATION:
FIRED Stam, Lynn
APPLICANT: Stam, Lynn
APPLICANT: Bacadus, Julie
APPLICANT: Bacadus, Julie
APPLICANT: Bacadus, Julie
APPLICANT: Bacadus, Julie
APPLICANT: Bacadus, Lynn
APPLICANT: BACATION NUMBER: US/10/108,605
CURRENT APPLICATION NUMBER: US 60/761,142
PRIOR FILING DATE: 2001-01-14
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SEG ID NO 227
LENGTH: 465
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                                                   79.5%; Score 31; DB 16; Length 313;
55.6%; Pred. No. 1e+02;
ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 130, Application US/10004378A Publication No. US20030228301A1 GENERAL INFORMATION:
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; ORGANISM: Drosophila melanogaster .
US-10-108-605-227
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Furtak, Kazarzyna
Perna, Amanda
Patturajan, Meera
Shimkets, Richard A
Guo, Xiaola Josha
Guo, Xiaola Josha
Rugess, Catherine E
Malyankar, Uriel M
Tchernev, Velizar T
Vernet, Corrine A
Spytek Kimberly A
Agee, Michele
Rastelli, Luca
Shenoy, Suresh G
Grosse, William M
Alsobrook II, John P
Lepley, Denlise M
Gerlach, Valerie
Bdinger, Schlomit
MacDougall, John R
Peyman, John R
Peyman, John R
Peyman, John R
Gunther, Erik
                                                   Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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US-10-004-378A-130
                                                                                                                                                                                                                                                                                                                                  RESULT 10
US-10-108-605-227
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  Gaps
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; OTHER INFORMATION: Xaa represents any amino acid at this position.
(92-10-032-950-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                          APPLICANT: Mair, Tom
APPLICANT: Mayville, Patricia
APPLICANT: Mayville, Patricia
APPLICANT: Beavis, Ronald
APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/10/032,950
GURRENT FILING DATE: 2001-12-27
PRICR APPLICATION NUMBER: 66/190,402
PRICR FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 29; DB 15; Length 55; Pred. No. 42; 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 29; DB 13; Length 9;
Pred. No. 1.2e+06;
0; Mismatches 1; Indels
Indels
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US-10-424-599-242903
  ä
  Mismatches
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88.9%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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     6; Conservative
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GVNAXSSLF 9
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Best Local Similarity
Matches 6; Conserva
                                                       2 VNAXSSLF 9
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     Matches
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                                                                   APPLICANT: BLIEFILM, ANGLE AN A TITLE OF INVENTION, No. US2003028301A1e1 Human Proteins, Polymucjectides Encoding Th TITLE OF INVENTION: No. US2003028301A1e1 Human Proteins, Polymucjectides Encoding Th TITLE OF INVENTION: No. Wethods of Using the Same FILE APPLICATION NUMBER: US/10/004,378A

CURRENT PELING DATE: 2001-10-24

PRIOR PLING DATE: 2000-10-24

PRIOR PLING DATE: 2000-10-26

PRIOR PLING DATE: 2000-10-36

PRIOR PLING PRIOR PLING DATE: 2000-10-36

PRIOR PRIOR PLING DATE: 2000-10-36

PRIOR PRIOR PRIOR PLING DATE: 2000-10-36

PRIOR PRIO
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Sequence 6225, Application US/10369493

Publication No. US2030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

APPLICANT: Gldman, Barry S.

APPLICANT: Glodman, Barry S.

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION PLANTS WITH IMPROVED PROPERTIES

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 6225

LENGTH. 632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 30; DB 14; Length 465;
Pred. No. 2.6e+02;
1; Mismatches 2; Indels
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Pred. No. 3.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
                                  Stone, David J
Ellerman, Karen
Gangolli, Esha A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            339 GVNLFSSIF 347
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Best Local Similarity
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Wed Oct 27 09:38:08 2004

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1 GVNAXSSLF 9 || | : || | 23 GVEATTSLF 31

Search completed: October 26, 2004, 16:10:09 Job time : 32.5 secs

QC

us-10-032-950-1.rpr

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 26, 2004, 15:46:55; Search time 8.73529 Seconds (without alignments) 99.132 Million cell updates/sec Run on:

US-10-032-950-1 39 1 GVNAXSSLF 9 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	AgrD protein (impo	lysosomal membrane	P2B/LAMP-1 precurs	둤	ferrichrome ABC tr	receptor-protein k	kpsD_protein - Esc	probable polysacch	phosphotransferase	SEC24 protein - ye	റ.	uga	probable beta-gluc	hypothetical prote	101	protein M homolog	mannitol-1-phospha	mannitol-1-phospha	hypothetical prote	880	ubiquinol-cytochro	zip protein precur	e ext	protein Y32F6A.3 [hypothetical prote		thy]	급	cal
	ID	C833	A2806	A6053	A3020	C6981	T4578	83665	E81286	D6975	S4846	A9922		T0240	T2721	S5843	B4371	AH097	B6516	F8505	A3195	ZPBOC		AB018	G8918	T0153	T2602	A3023		AF255
	Length DB		82	0.5	07	33	95	68	394 2	31	56	60	20	09	33	69	69	82	82	98	16	53	00	18	55	46	63	054	1435 2	m
þ	Query Match L	 92.3	σ,	89.7	σ,	87.2	ď	σ.	79.5	σ,	<u>ი</u>	ů.	ė.	9	76.9	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4		ä
	Score	 36	35	35	35	34	32	31			31	30	30	30	30	29	53	29	29	29	29	29	29	29	59	29	29	50	53	28
	Result No.	ri	7	m	4	ıń	9	7	80	σ	10	11	12	13	14														28	

hypothetical prote probable galactosy iron(III) dicitrat hypothetical prote ubiquinol-cytochromaltose/maltodextr manganese transpor hypothetical prote	Similar to Cytochr hypothetical prote beta-glucosidase-1 conserved hypothet conserved hypothet peptidase (M3 fami
F90350 S55491 S74439 A5324 S12023 C70038 C83902 AF2539	D86306 C96744 T47837 F64640 F82236 F81313
0 0 0 0 0 0 0 0 0 0 0	000000
2 E E E E E E E E E E E E E E E E E E E	444 0448 0448 0589 7389
7717.88	71.8 71.8 71.8 71.8 71.8
8888888888 777777777777777777777777777	888888
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ALIGNMENTS

RESULT 1
Dark Darkein (immorted) - Stanbylococcis aureus (strain N315)
gn
C;Date: 10-May_2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004 C:Accession: C89995
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A; Accession: (189995)
A;Status: preliminary
A; Molecule type: DNA
A; Cross-references: UNIPROT:033586; GB:BA000018; PID:g13701831; PIDN:BAB43124.1; GSPDB:
A;kxperimental source: strain N315 C;Genetics:
A;Gene: agrD
atch 92.3%; Score 36; DB 2; Length 47; cal Similarity 88.9%; Pred. No. 0.11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GVNAXSSLF 9
Db 24 GVNACSSLF 32
RESULT 2
lysosomal membrane glycoprotein LAMP-1 - mouse
C;bpecies: Mus musculus (mouse mouse) C;bate: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C,Accession: A28067
R. K.
A; Title: Isolation and sequencing of a cDNA clone encoding lysosomal membrane glycoprot
Ajkererence number: Az808/j MOID:88243/32j FMID:33/3044 AjAccession: A28067
A;Molecule type: mRNA A:Regidings: 1-382 cCHR>
A; Cross_referous: UNINFROT:F11438; GB:J03881; NID:g198706; PIDN:AAA39411.1; PID:g29369 A; Cross_referous: UNINFROT:F11438; GB:J03881; NID:g198706; PIDN:AAA39411.1; PID:g29369
C;Superfamily: lysosome-associated membrane protein C;Keywords: glycoprotein; membrane protein
Match 89.7%;
best Local Similarity (7.8%) Fred. NO. 1.5% Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Accesion: C6912
B;Kunst, F:; Ogasawara, N:; Moszer, I:; Albertini, A.M.; Alloni, G:; Azevedo, V:; Berter, B: Bron, S:; Brougar, S:; Bruschi, C.V.; Caldwell, B:; Capuano, V:; Carter, N.M.; Cho. A.; Brust, S.; Brung, S.; Galder, C.; Frighta, M.; Fulla, V.; Fuma, S.; Galizzi, A.; Galler, A.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Hundors: Lauber, J.; Lazrevic, V.; Lee, S.M.; Levile, H.; Manda, S.; Maueell, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Darro, J.; Parzo, T.; Scanlon, A.; Anthors: Schlack, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sexoo, T.; Scanlon, A.; Hamakoshi, A.; Tareptara, P.; Tognoni, A.; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A)Cross references: UNIPROT:034933; GB:Z99108; GB:AL009126; NID:g2633055; PIDN:CAB12580.
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laudie, M.; Mewes, H.W.; Lemcke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     836553
kpsb protein - Escherichia coli
C;Species: Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor-protein kinase-like protein - Arabidopsis thaliana
NiAlternate names: protein P26013.190
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Species: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 16-Aug-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 333;
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A,Experimental source: cultivar Columbia; BAC clone F26013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C)Accession: T45786
R;Delseny, M.; Berger, C.; Cooke, R.; Grellet, F.; Laudie, submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23013
A;Accession: T45786
A;Accession: preliminary
A;Acture: preliminary
A;Molecule type: DNA
A;Residues: 1-895 <DEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.2%; Score 34; DB 1;
77.8%; Pred. No. 2.8;
tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: yfmD
C,Superfamily: ferrichrome ABC transporter
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A,Note: F26013.190
C,Superfamily: protein kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 GVNAGASLF 107
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Best Local Similarity
Matches 7; Conserv
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Matches
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N.Alternate names: sialoglycoprotein
C;Species: Rattus norvegicus (Norway rat)
C;Accession: A30200; S0331
R;Howe, C.L.; Granger, B.L.; Hull, M.; Green, S.A.; Gabel, C.A.; Helenius, A.; Mellman,
Proc. Natl. Acad. Sci. Us.A. 85, 7577-7581, 1988
A;Title: Derived protein sequence, oligosaccharides, and membrane insertion of the 120-k
A;Reference number: A30200, MUID:89017240; PMID:3174652
A;Accession: A30200
A;Molecule type: mRNA
A;Residues: 1440 AMDA
A;Cross references: UNIFROT:P14562; EMBL:003672
A;Note: the authors translated the codon GGG for residue 15 as Val
A;Note: the authors translated the codon GGG for residue 15 as Val
A;Note: the authors translated the codon GGG for residue 15 as Val
A;Note: the authors translated the codon GGG for residue 15 as Val
A;Note: the authors translated the codon GGG for residue 15 as Val
A;Note: the authors translated the codon GGG for residue 15 as Val
A;Note: the authors translated the codon GGG for residue 15 as Val
A;Note: the authors translated the codon GGG for residue 15 as Val
A;Note: the authors translated the codon GGG for residue 15 as Val
A;Note: the authors translated the codon GGG for residue 15 as Val
A;Note: the authors translated the codon GGG for translated the mature protein in A;Residues: 22-407 AHID:
A;Note: part of this sequence, including the amino end of the mature protein in A;Residues: 22-407 AHID:
A;Note: part of this sequence, including the amino end of the mature protein c;Superfamily: lysosome-associated membrane protein
C;Superfamily: lysosome-associated membrane protein, 107K #status experimental AMAT>
                                                                                                                                                                                                                                                        A6054.

P2B/LAWP-1 precursor - mouse
P2B/LAWP-1 precursor - mouse
P2B/LAWP-1 precursor - mouse
P2B/LAWP-1 precursor - mouse
C;Species: Mus wasculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: A60534 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: A60534 #sequence_revision of P2B/LAMP-1, a major protein target of a metastasi
A;Reference number: A60534; MUD:90002989; PMID:2676155
A;Reference number: A60534; MUD:90002989; PMID:2676155
A;Reference number: A60534; MUD:90002989; PMID:2676155
A;Residues: 1-405 - HEF>
A;Residues: 1-405 - HEF>
A;Residues: 1-405 - HEF>
A;Residues: 1-405 - HEF>
A;Cross-references: UNIPROT:P11438
C;Superfamily: lysosome-associated membrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89.7%; Score 35; DB 2; Length 405; 77.8%; Pred. No. 2; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89.7%; Score 35; DB 2; Length 407; 77.8%; Pred. No. 2; 1; Mismatches 1; Indels
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120% lysosomal membrane glycoprotein precursor - rat
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Conservative
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                                                                                               256 GMNASSSLF 264
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                  1 GVNAXSSLF 9
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Best Local Similarity
7; Conserve
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phosphotransferase system enzyme II homolog ybfs - Bacillus subtilis
C;Becias: Bacillus subtilis
C;Beciasion: Boffs
R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte.
C; Bron, S.; Broullet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Erlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, K.; Lana, K.; Galizzi, A.; Galle;
iech, J.; Koningstein, G.; Krodh, S.; Kunano, M.; Kurita, K.; Lapidus, A.; Lardinois
Koetter, P.; Koningstein, G.; Krodh, S.; Roche, M.; Sadaie, Y.; Barno, S.; Hullo, M.F
Koetter, P.; Koningstein, G.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Sato, M.; Masuda, S.; Mauee
y, M.; Ogawa, K.; Ogiwara, A.; Oudeag, B.; Rose, M.; Sadaie, Y.; Sato, T.; Sekowska, A.; Sato, T.; Winters: Schletch, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero
akeuchi, M.; Tamakoshi, A.; Tamaka, T.; Terpstra, P.; Tognoni, A.; Tosato, T.; Scanlon
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Atthors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Atthors: Preliminary; nucleic acid sequence not shown; translation not shown
A;Accession: D69750
A;Coession: D69750
A;Coession: D69750
A;Coession: D69750
A;Coession: Local «KNU»
A;Roserimental source: strain 168
A;Gone Lices
C;Generices: UNIPROT: P39816; GB:Z99105; GB:AL009126; NID:g2632457; PIDN:CAB12029
A;Gone Lices
C;Generices: UNIPROT: P108044033; PALD:G126; NID:g2632457; PIDN:CAB12029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cypecies: Saccharomyces cerevisiae
Cypecies: Saccharomyces cerevisiae
Cypecesion: 484643
Rybowman, S., Churcher, C.
submitted to the EMBL Data Library, September 1994
AyReference number: 848455
AyResidues: 1-926 < BON>
AyResidues: 1-926 < BON>
AyCoss.references: UNIPROT:P40482; GB:Z47047; EMBL:Z38125; NID:g603997; PID:g763237; GCGenetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: ybfS
C;Superfamily: phosphotransferase system N-acetylglucosamine-specific enzyme II; phosph
nzyme II, factor III homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Pred. No. 31;
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A;Cross-references: MIPS:YIL109c; SGD:S0001371
A;Map position: 9L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.5%;
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Best Local Similarity 75...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 GINAASSL 179
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Cispecies: Campylobacter jejuni
Cispecies: Campylobacter jejuni
Cipate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
Cipate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
Cipate: 31-Mar-2000
Cipate: 31-Mar-2000
Cipate: 31-Mar-2000
Cimit Win Bailandream, M.A.; Rutherford, R.M.; Canurcher, C.; Basham, D.; Chillin
Cim.; Quail, M.; Rajandream, M.A.; Rutherford, R.M.; Canurcher, C.; Basham, D.; Chillin
Cim.; Quail, M.; Rajandream, M.A.; Rutherford, R.M.; Canurcher, C.; Basham, D.; Chillin
Althory Sequence of the food-borne pathogen Campylobacter jejuni reveals hype A; Reference number: A81256
A; Accession: E8126
A; Accession: E8126
A; Anchoral Cipate: DA
A; Residues: 1-394 *CPAR-A; CPAR-A; CPA
                                                                                                                                                                                         A, Status: preliminary
A, Molecule type: DNA
A, Molecule type: DNA
A, Molecule type: DNA
A, Molecule type: DNA
A, Rossiudes: 1-389
A, Cross-references: UNIPROT: P42218; EMBL: X74567; NID: 9397404; PIDN: CAA52659.1; PID: 93974
A, Cross-references: UNIPROT: P42218; EMBL: X74567; NID: 9397404; PIDN: CAA52659.1; PID: 93974
B, Pazzani, C.; Rosenow, C.; Boulnois, G.J.; Bronner, D.; Jann, K.; Roberts, I.S.
A, Title: Molecular analysis of region 1 of the Escherichia coli K5 antigen gene cluster: A, Reference number: A48492; MUID: 93388530; PMID: 8397187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Accession: C42644
A, Status: preliminary
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 106-125, 'D', 127-244, 'N', 246-297, 'S', 299-300, 'VI', 303-379, 'M', 381-385, 'W', 387
A, Erosa-references: GB, MTG370, 'N ID: 416947, PIDN: AAA24214.1; PID: 9146950
A, Experimental source: K1, strain EVI
A, Note: sequence extracted from NCBI backbone (NCBIN: 79370, NCBIP: 79381)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A)Status: preliminary
A,Molecule type: DNA
A,Molecule type: DNA
A,Esidues: 22-389 <-PAZ>
A,Cross-references: GB:X74567
A,Cross-references: GB:X74567
A,Cross-references: GB:X74567
A,Title: Functional analysis of the sialyltransferase complexes in Escherichia coli K1
A,Reference number: A42644; MUID:92138601; PMID:1735705
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Pred. No. 18;
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Pred. No. 18;
0; Mismatches
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                                            R,Roberts, I.S.
submitted to the EMBL Data Library, August 1993
Reference number: S36649
A,Accession: S36653
C; Accession: S3653; E48492; C42644 R; Roberts, I.S.
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Best Local Similarity 8/...
7; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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A,Gene: kpsD
C,Superfamily: kpsD protein
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C;Superfamily: kpsD protein
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Rylin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; W.; Koo. H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Viernam, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A.Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A.Reference number: A84420; MUID:20083487; PMID:10617197
A.Accession: B84879
A.Accession: B84879
A.Residues: DNA
A.Residues: 1-560 <STO>
A.Residues: 1-560 <STO>
A.Cross-references: GB:AE002093; NID:93128191; PIDN:AAC16095.1; GSPDB:GN00139
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A;Cross-references: UNIPROT:018227; EMBL:299281; PIDN:CAB16503.1; GSPDB:GN00022; CESP:YS
A;Experimental source: clone Y57G11C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:090655; EMBL:U25353; NID:9857681; PIDN:AAA83567.1; PID:g8576
R;Ryan, A.K.; Tejada, M.L.; May, D.L.; Dubaova, M.; Deeley, R.G.
Nucleic Acids Res. 23, 3252-3259, 1995
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NyAlternate names: avian knotted-related protein; homeotic protein AKR
Cispecies: Gallus gallus (chicken)
Cibate: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Aug-2004
CiAccession: S58439; S58440
Rixyan, A.K.; Tejada, M.L.; May, D.L.; Dubaova, M.; Deeley, R.G.
Rixyan, A.K.; Tejada, M.L.; May, D.L.; Dubaova, M.; Deeley, R.G.
A;Description: Isolation and characterization of the chicken homeodomain protein AKR.
A;Reference number: S58439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Map position: 2
A, Introns: 3/2; 33/3; 76/3; 102/1; 157/2; 242/3; 281/2; 354/1; 400/1; 438/2
C, Superfamily: Agrobacterium beta-glucosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein Y57G11C.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 09-Jul-2004
C;Accession: T27215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Introns: 70/1; 329/3
C,Superfamily: multidrug resistance protein; ATP-binding cassette homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Length 560;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R,McMurray, A. submitted to the EMBL Data Library, September 1997 A;Reference number: 220330 A;Accession: T27215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 30; DB 2
Pred. No. 47;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 76.9%;
Similarity 66.7%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322 GINYYSSLF 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Gene: At2g44490; F4I1.30
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Best Local Similarity
Matches 6, Conserv
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A; Residues: 1-269 <RYA>
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A;Gene: CESP:Y57G11C.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable sugar-binding protein YPO0856 [imported] - Yersinia pestis (strain CO92)
c; Species: Versinia pestis
C; Species: Versinia pestis
C; Species: Versinia pestis
C; Species: Versinia pestis
C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C; Accession: AD0105
R; Parkfill, J., Wir Davis, Davi
hypothetical protein SS00775 [imported] - Sulfolobus solfataricus
C;Gpecies: Sulfolobus solfataricus
C;Gpecies: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: A99227
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chandong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Cost, J.
Abescription: Sulfolobus solfataricus complete genome.
A;Accession: A99227
A;Accession: A99227
A;Accession: A99227
A;Accession: Apper: DNA
A;Residues: 1-109 <KUR>
A;Residues: 1-109 <KUR>
A;Gross-references: UNIPROT:Q9UXG2; GB:AE006641; NID:g13813950; PIDN:AAK41072.1; GSPDB:G
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TOO 2404

Drobable beta-glucosidase homolog F4I1.30 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Os Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02404; B84879
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul Submitteed to the BMED Data Library, May 1998
A;Poescription: Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence.
A;Reference number: 214667
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-560 <ROLD-
A;Residues: 1-560 <ROLD-
A;Cross-references: UNIPROT:O64883; EMBL:AC004521; NID:g3128166; PIDN:AAC16095.1; PID:g3
A;Experimental source: cultivar Columbia
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GLNAIDSLF 256
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Matches 5; Conserv
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A;Title: Isolation and characterization of the chicken homeodomain protein AKR.
A;Accession. SS8440; MUID:95396587; PMID:7667102
A;Accession. SS8440.
A;Scatus: nucleic acid sequence not shown
A;Scatus: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 35-94 *RYFF>-
A;Cross-references: EMBL:U25353
C;Function:
A;Description: negative regulator of apoVLDLII (major egg yolk apolipoprotein)
A;Description: negative regulator of apoVLDLII (major egg yolk apolipoprotein)
A;Note: expressed in liver during early embryogenesis and in non-hepatic adult tissues
C;Superfamily: homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;36-95/Domain: homeobox homology < HOX>
C;Keywords: DNA binding; homeobox nonlogy < HOX>
C;Keyword
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Search completed: October 26, 2004, 16:06:05 Job time : 10.7353 secs

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Cae26182 rhodopseu P39816 bacillus su O91aw0 mycoplasma Q75b16 ashbya goss Aas51681 ashbya go P40482 saccharomyc O9uxg2 sulfolobus (899v1 bradyrhizob Q78br1 carassius a Q737n6 bacillus ce Aas41526 bacillus G6hic7 bacillus G6hic7 bacillus C6hic7 bacillus 
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STRAIN=SA502A;
MEDLINE=97342847; PubMed=9197262;
Ji G., Beavis R., Novick R.P.;
"Bacterial interference caused by autoinducing peptide variants.";
Science 276:2027-2030(1997).
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STRAIN=CH31a-cp5, Gt31b-cp5, Gt36a-cp8, Gt36b-cp8, and Gt111-cp8;
Goerke C. Dasbacds S., Kluemmel M., Wolz C.;
Submitted (DEC-2003) to the BMBL/GenBank/DDBJ databases.

EMBL; AP001782; AAB63265.1; -.
EMBL; AJ617715; CAE92748.1; -.
EMBL; AJ617717; CAE92754.1; -.
EMBL; AJ617717; CAE92754.1; -.
EMBL; AJ617719; CAE92757.1; -.
EMBL; AJ617719; CAE92757.1; -.
EMBL; AJ617719; CAE92757.1; -.
EMBL; AJ617719; CAE92757.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
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Pred. No. 1;
0; Mismatches
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CAE26182
YBFS BACSU
Q9LAW0
Q75B16
AAS51681
SC24 YEAST
Q9UXG2
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AAS41526
Q6HIC7
Q7Z8M2
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Q78BR1
Q98SE3
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Best Local Similarity 88.9%;
Matches 8; Conservative
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      24 GVNACSSLF 32
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SEQUENCE 47 AA; 51
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      AgrD.
Name=agrD;
      033586;
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033586
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Q7A2N4
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bordetella
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(without alignments)
127.445 Million cell updates/sec
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P49129 c
Q8ev24 m
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                      5.1.6
Compugen Ltd.
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                      GenCore version (c) 1993 - 2004
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07A2N4
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Q94C93
Q94C93
Q47C98
Q7VGP8
KSS5 ECOLI
CAEXCZ9
Q9PMP4
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Q8EV24
Q8FDP8
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SEQUENCE FROM N.A.
STRAIN-gt31a-cp5,
Goorke C., Dasbach S., Kuemmel M., Wolz C.;
Goorke C., Dasbach S., Kuemmel M., Wolz C.;
and cap in Staphylococcus aureus.";
submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, A.617715; CAE92745.1, -.
SEQUENCE 47 AA, 5149 MW; 22893764DF54BFA7 CRC64;
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Goerke C., Dasbach S., Kuemmel M., Wolz C.;
"Evolutionary Models for the Development of the Polymorphic Loci agr
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NCBI_TaxID=1280;
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Bacteria, Firmicutes, Bacillales, Staphylococcus.
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Best Local Similarity 88.30,
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8; Conservative
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Matches 8; Conservative
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MEDLINE=21311952; PubMed=11418146;

Kuroda M., Ohta T., Uchiyama I., Yazawa H., Kobayashi I.,

Kuroda M., Ohta T., Uchiyama I., Lian J.-Q., Ito T.,

Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

Kanamori M., Takahashi N.K., Sawan T., Inoue R.-I., Kaito C.,

Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

"Whole genome sequencing of meticillin-resistant Staphylococcus

ureus."
                                                                                                                MEDLINE=21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekinizu K., Hirakawa H., Khibara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hatcori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
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Pred. No. 1;
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Bacteria; Frimicues; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22893764DF54BFA7 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Bacteria; Firmicutes; Bacillales; Staphylococcus
NCBI TaxID=158878;
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EMBL, AP003364; BAB58199.1; -.
InterPro, IPR009229; AgrD.
Ffam; PF05931; AgrD; 1.
Complete proteome.
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EMBL, APRO03135; BAR43124.1; -.
InterPro; IPR009229; AgrD.
Pfam; PF0S931; AgrD; 1.
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STRAIN-gt36a-cp8;
Goerke C., Dasbach S., Kuemmel M., Wolz C.;
"Bvolutionary Models for the Development of the Polymorphic Loci agr and cap in Staphylococca auxeus,";
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ617717; CAE92751.1;
SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=gt36b-cp8;
Goerke C., Dasbach S., Kuemmel M., Wolz C.;
"Foolutionary Models for the Development of the Polymorphic Loci agr and cap in Staphylococca aureus.",
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ617718; CAE92754.1; -..
SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;
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STRAIN=gtll1-cp8;
Goerke C., Dasbach S., Kuemmel M., Wolz C.;
Goerke C., Dasbach S., Kuemmel M., Wolz C.;
and cap in Staphylococcus aureus.";
submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ617719; CAB92757.1; -.
SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;
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01-APR-2004 (TrEMBLrel. 27, Last sequence update)
01-APR-2004 (TrEMBLrel. 27, Last annotation update)
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Last sequence update)
Last annotation update)
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Bacteria, Firmicutes, Bacillales, Staphylococcus.
NCBI_TaxID=1280;
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NCBI_TaxID=1280;
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Pred. No. 1;
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                                                                                                                                                                                           Local Similarity 88.9
les 8; Conservative
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Matches 8; Conservative
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CAE92754;
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausberg R.L., Schouler G.D.,

Ray Altschul S.F., Zeeberg B. Buecow K.H., Schaefer C.F., Bhat N.K.,

Ray Hopkins R.F., Jordan H., Moore T., Max S.I!, Wang J., Hsieh F.,

Blackbenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,

Ray Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

Ray Ray S.A., McDwan B., Deters G.J., Abramson R.D., Mullahy S.J.,

Ray Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Ray Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glubs R.A.,

Ray Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glubs R.A.,

Ray Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Ray Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Ray Nordiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Ray Jones S.J., Marra M.A.;

Ray Mones S.J., Marra M.A.;

Ray Green E.D., Dickson M.C., Schein J.E.,

Ray Jones S.J., Marra M.A.;

Ray Green E.D., Myers R.M., Schein J.E.,

Ray Jones S.J., Marra M.A.;

Ray Green E.D., More C., Ashinki A., Schein J.E.,

Ray Green E.D., More C., Grimban J.E.,

Ray Jones S.J., Marra M.A.;

Ray Rederation and initial analysis of more than 15,000 full-length human
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TISSUE-Mammary tumor metastatized to lung. Tumor arose spontaneously;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxIb=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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Submitted (APR. 2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006785; A4H06785.1; -.
MGD; MGI:96745; Lampl.
GO; GO:0005764; C:lysosome; IDA.
GO; GO:0005771; C:multivesicular body; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 189 AA; 20456 MW; 71F16D69BA4066FA CRC64;
                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Pred. No. 7.9;
1; Mismatches
                                                                                                                                                                                   189 AA
                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                   PRT;
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PROSITE; PS00310; LAMP 1; 1.
PROSITE; PS00311; LAMP 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA sequences."
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Pfam; PF01299; Lamp; 1.
                                                                                                                                                                                                                                                                                                                                                           Lampl protein (Fragment).
Name=Lampl;
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24 GVNACSSLF 32
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                                                                                                                  Pfam, PF01299; Lamp; 1.
PRINYE; PR00336; LYSASSOCTDMP.
SS00310; LAMP 1; 2.
PROSITE; PS00311; LAMP 2; 1.
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77.8%;
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                                                                                                         EMBL; M25244; AAA39869.1; -.
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406 AA;
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Q8VH34
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MEDINE-2518L/6; TISSUE-Brain;

MEDINE-2518L/6; PubMed=12477932; DOI=10.1073/pnas.242603899;

MALTAUSDER R.D., Colling R.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wabin G.M., Heish F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Medicul R., Schein J.B., Jones S.J.M., Marra M.A.,

R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDILINE=90237040; PubMed=2332434;
Arterburn L.M., Earles B.J., August J.T.;
"The disulfide structure of mouse lysosome-associated membrane protein
                      Chen J.W., Cha Y., Yuksel K.U., Gracy R.W., August J.T., Isolation and sequencing of a CDNA clone encoding lysosomal membrane glycoprotein mouse LAMP-1. Sequence similarity to proteins bearing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Presents carbohydrate ligands to selectins. Also implicated in tumor cell metastasis.
SUBCELLULAR LOCATION: Type I membrane protein. Lysosomal. This protein shuttles between lysosomes, endosomes, and the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: O- and N-glycosylated; some of the N-glycans attached to LAMP-1 are polylactosaminoglycans (By similarity). SIMILARITY: Belongs to the LAMP family.
                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                  "Characterization and cloning of lgp110, a lysosomal membrane glycoprotein from mouse and rat cells.", Biol. Chem. 265:12036-12043(1990).
                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-90307738; PubMed=2142158;
Granger B.L., Green S.A., Gabel C.A., Howe C.L., Mellman I.,
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Heffernan M., Yousefi S., Dennis J.W.;
Submitted (FEB-1990) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 25-406 FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=88243732; Pubmed=3379044;
              406 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Chem. 263:8754-8758(1988).
               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.
               STANDARD;
                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                 NCBI_TaxID=10090;
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               MOUSE
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Pred. No. 18;
1; Mismatches 1; Indels
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First lumenal domain.
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Second lumenal domain.
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V -> I (in R
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N-linked
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE-89017240; PubMed=3174652;
Howe C.L., Granger B.L., Hull M., Green S.A., Gabel C.A., Helenius A.,
Mellman I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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-I-SUBCELLULAR LOCATION: Type I membrane protein. Lysosomal. This protein shuttles between lysosomes, endosomes, and the plasma
                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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MEDIATE=89153580; PubMed=22920835;
Himeno M., Noguchi Y., Sasaki H., Tanaka Y., Furuno K., Kono Sakaki Y., Kato K.;
"Isolation and sequencing of a cDNA clone encoding 107 kDa sialoglycoprotein in rat liver lysosomal membranes.";
FEBS Lett. 244:351-356(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 2; Length 406;
Pred. No. 18;
1; Mismatches 1; Indels
                                                                                                                                                                              Ono K., Han J.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, ANG69964 AAL58070.1; -.
GO, GO:0005764; Lampl.
GO, GO:0005771; C:mlltivesicular body; IDA.
GO, GO:00047383; C:sarcolemma; IDA.
InterPro; IRR002000; Lamp.
PF01299; Lamp; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Lysosome-associated membrane glycoprotein 1 precursor (Some 1 ysosomal membrane glycoprotein) (LGP-120) (CD107A)
Name=Lampl; Synonyms=Lamp-1;
                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00336; LYSASSOCTDMP.
PR0SITE; PS00310; LAMP 1; 2.
PR0SITE; PS00311; LAMP 2; 1.
SEQUENCE 406 AA; 43879 MW; C1BD373548ADFA85 CRC64;
 Last sequence update)
Last annotation update)
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77.8%;
01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2004 (TrEMBLrel. 26,
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                                                                    Mus musculus (Mouse).
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P14562; P97620;
01-JAN-1990 (Re]
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                 Lysosome-associated membrane glycoprotein
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PTM: O- and N-glycosylated; some of the N-glycans attached to LAMP-1 are polylactosaminoglycans (By similarity). SIMILARITY: Belongs to the LAMP family.
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Pred. No. 18;
1; Mismatches 1; Indels
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25947490749A7C88 CRC64;
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C STRING-STBL/GG; TISSUE-Lung;
A Arakawa T., Boro H., Carning;
A Arakawa T., Boro H., Carning;
A Hanagaki T., Hara A., Hayatsu N., Hiracka T., Hori F.,
A Hanagaki T., Hara A., Hayatsu N., Hiracka T., Hori F.,
A Matsuyama T., Myazaki A., Nashi K., Nomura K., Numazaki R., Ohno M.,
A Matsuyama T., Myazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Sakai C.,
A Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
A Sano H., Sasaki D., Yagami M., Tagawa A., Takahashi F., Tanaka T.,
A Sabbat Y., Toya T., Yamamura T., Yasunishi A., Yoshino M.,
Muramatsu M., Hayashizaki Y., T., Yasunishi A., Yoshino M.,
B Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databasee.
R EMBL, AKO04637; BARZJ4281; -.
R MGD; MGI:96745; Lampl.
                                                                                                                                                                                                                                                                                                                                                                                                                          The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
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                                           enriched library,
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MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matamioto H., Sakaguchi S., Inegami T., Rashiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka M., Ohara B., Matahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rikk integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Lung;
MEDLINE-21085660; PubMed-11217851;
MIEDN FANTOM CONSORTIUM;
"FUNCTIONAL ANDOLATION of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male lung cDNA, RIKEN full-length enriched lik
clone:1200007101 product:lysosomal membrane glycoprotein 1, full
                                                                                                                                                                                                                             Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=99279253; PubMed=10349636;
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STRAIN=C57BL/6J; TISSUE=Lung;
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RA Azevedo V., Berrero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Berrero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Bourise K., Baursier L., Brans A., Braun M., Brighell S.C., Bron. S.,
RA Brouilet S., Bruschi C.V., Candwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Godni J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Entian K.-D., Errington J., Pabret C., Ferrari B., Founger D.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Klaerr-Blanchard M.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Klaerr-Blanchard R.,
R. Jones L.M., Ooris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
RA Klein C., Medina M., Moeiter P., Koningstein G., Krogh S.,
RA Medigue C., Medina M., Mallado R.P., Liu H., Masuda S., Mauel C.,
RA Medigue C., Medina M., Mallado R.P., Mizuno M., Moesell D., Nakai S.,
RA Porsoctt A.M., Prescen E., Pulic P., Purnelle B., Rapoport G.,
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA Scoffone F., Sekiguchi A., Tacconi B., Takahashi H.,
RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Takahashi H.,
RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Takahashi H.,
RA Vasaarotti A., Viari A., Wambut R., Wedler E., Wedler E., Wedler E.,
RA Weitzenegger Y., Winters P., Winders P., Wamane C., H., Yoshikawa H., Pannone P., Wamaner P., Yamane K., Yoshikawa H., Pannone P., Wanner P., Wanner P., Wanner R., Wentzenegger Y., Wanner P., Yamane A., Yannane C., Wanner M., Yashikawa H., Panner M., Yashikawa H., Panner M., Yashikawa H., Panner M., Wanner M., Wanner
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MEDLINE=97417489; PubMed=9272861;
Yamamoro H., Uchiyama S., Nugroho F.A., Sekiguchi J.;
Yamamoro H., Uchiyama G., Nugroho F.A., Sekiguchi J.;
"Cloning and sequencing of a 35.7 kb in the 70 degree-73 degree region "Cloning and sequencing of a 35.7 kb in the 70 degree-73
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GO; GO:0005764; C:lyBosome; IDA.
GO; GO:0005771; C:multivesicular body; IDA.
GO; GO:0042383; C:sarcolemma; IDA.
FOR PROSCOO; Lamp.
PRINTS; PR01299; Lamp; 1.
PRINTS; PR03316; LYSASSCTDMP.
PROSITE; PS00310; LAMP_1; 2.
PROSITE; PS00311; LAMP_2; 1.
SEQUENCE 407 AA; 43936 MW; 696D0C79F627DA84 CRC64;
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MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             034933; Q79ET2;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YfmD protein.
Name=yfmD; OrderedLocusNames=BSU07510;
Bacillus subtilis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 77.8
Matches 7; Conservative
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of the Bacillus subtilis genome reveal genes for a new two-component system, three spore germination proteins, an iron uptake system and a general stress response protein.";

Gene 194:191-199 (1997).

EMBL; 299108; CAB12580.1; -.

EMBL; 299108; CAB12580.1; -.

BIRL; D86417; BAA22318.1; -.

BIRL; D66019; CAB12580.1; -.

GO; GO:0016202; C:nembrane; IEA.

GO; GO:0005215; F:transporter activity; IEA.

GO; GO:0005215; F:transport; IEA.

InterPro; IPR000522; FeCD.

Fram; PFD01032; FeCCD; 1.
                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIJUNE=21137858; PubMed=11240104;
MEDIJUNE=21137858; PubMed=11240104;
Hayakawa Y.;
Hayakawa Y.;
Wariation of the agr locus in Staphylococcus aureus isolates from variation of the agr locus in Staphylococcus aureus isolates from Vet. Macrobiol. 79:267-274(2001).
EMBL; AB043554; BAB18547.1; -.
InterPro; IPR009229; AgrD.
Pfam; PP05931; AgrD; 1.
SEQUENCE 46 AA; 5050 MW; 404714CDC4BFA77E CRC64;
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 77.8%; Pred. No. 8.7;
Matches 7; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                        333 AA; 35098 MW; 9F4BE91BB0EE6761 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       OFIUS;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
VOSI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                              46 AA
                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                   99 GVNAGASLF 107
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SEQUENCE 333 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=agrD;
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Q9F1U5
ID Q9F1U5
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Search completed: October 26, 2004, 16:04:54 Job time : 43.6324 secs

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Arabidops Arabidops Arabidops Arabidops Human sbg Protein e Herbicida Thale cre S. aureus S. aureus AgrD-auto AgrD-auto AgrD-auto Cyclic pe Cyclic pe

Aag61267 Aag61256 Aag61256 Abb80603 Abb80604 Abb80604 Abb9322 Aay67856 Aay67856

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This sequence represents a cyclic peptide derived from the Staphylococcus aureus AgrD peptide. The invention relates to AgrD derived peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New cyclic peptides for treating infections with Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "N-terminal residue forms bond with C-terminal residue to form a cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus infection; cyclic peptide; AgrD; agr response; virulence factor; treatment.

    aureus peptide #2 used for bacterial interference.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muir TW, Mayville P, Novick RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY67852 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Unknown
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(UYNY ) UNIV NEW YORK STATE.
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                                                                                                                                                                                                                                                                                                              222
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Misc-difference
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Modified-site
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  AAY67852;
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  Auge See Age S
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Cyclic pe
Staphyloc
Staphyloc
Peptide-m
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                                                                                                                          October 26, 2004, 15:44:15; Search time 42.75 Seconds (without alignments) 75.522 Million cell updates/sec
                GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                 2002273 seqs, 358729299 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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AAX67869
AAX67863
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AAM50900
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Gapop 10.0 , Gapext 0.5
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11: geneseqp1980s:*
2: geneseqp1990s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003s:*
6: geneseqp2003bs:*
8: geneseqp2003bs:*
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39
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Match Length
                                   Copyright
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Beavis R;

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SXSS

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Muir TW, Mayville P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MUIR/) MUIR T W.
(MAYV/) MAYVILLE P.
(NOVI/) NOVICK R P.
(BEAV/) BEAVIS R.
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                                                                                                                      Similarity
9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                         1 GANAXSSLF
                                                                                                                                                                               GANAXSSLF
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                                                                                       Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-DEC-2001;
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                                                                                                           Query Match
Best Local S
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                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of a novel synthetic cyclic peptide of the invention that is capable of inhibiting the agr response of staphylococcus aureue. It is an AgrD-autoinduring peptide, where AgrD is staphylococcus aureue. It is an AgrD-autoinduring peptide, where AgrD is secreted agr-encoded peptide and where the agr locus controls the synthesis of virulence factor and other extracellular proteins the sequence NH2-X(n)-Z-X(y)-COM, with a cyclic bond between the Z residue and COOH other than a thiosester bond, where X is an amino acid analogue, a peptidomimetic or non-amide isosters, Z is a namino acid analogue, a peptidomimetic or non-amide isosters, Z is a synthetic or a biosynthetic amino acid, n is 0-10 and y is 1-10. The cyclic bond is especially a lactam or lactone bond. The thiololactone structure within native AgrD peptides is required for activation of the structure can destroy agr response activating activity while preserving and enhancing inhibitory activity. A claimed method of preparing a cyclic
                                                                              ö
with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus
                                                                                                                                                                                                                                                                                                                                                                                                    /note= "note linked to residue 5 to form cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                       'note= "note linked to residue 9 to form cyclic peptide"
                                                                               Gaps
                                                                                                                                                                                                                                                                         Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic; antibacterial; infection; therapy; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in subject.
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                                                                                                                                                                                                                                                  AgrD-autoinducing cyclic peptide, inhibitor of agr response.
                                                        Length 9;
                                                                             Indels
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                                               DB 3; Le...
                                                 94.9%; Scor.
100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                                              'note= "any amino acid"
                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novick RP,
                                                                                                                                                                                   AAM50900 standard; peptide; 9 AA.
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                                                                                                                                                                                                                               (first entry)
                                                                               Conservative
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                                                                                                     σı
                                              Query Match
Best Local Similarity
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                                    Sequence 9 AA;
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peptide involves; assembling a linear peptide chain on to a solid phase resin support; deprotecting the resulting protected assembled peptide; treating the deprotected peptide with neutral buffer for a time sufficient to form the cyclic peptide and cleave the peptide from the support; and recovering the cyclic peptide. The peptide is useful for bacterial interference, especially for the treatment of S. aureus
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyclic peptide, Staphylococcus aureus; infection; antibacterial; agr response inhibitor.
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                                                                                                                                                                                                                                                                                      Score 37; DB 5; Length 9;
Pred. No. 1.7e+06;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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100.0%; Pred. No. 1.7e+06;
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                                                                                                                                                                                                                                                                     94.9%; Scc.
100.0%; Pre
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99US-00339511.
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Matches

AAY67860;

AAY67860

RESULT

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This sequence represents the Staphylococcus aureus AgrDII derived peptide. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus
                                                                                                                                                                                                                                                                                                                        New cyclic peptides for treating infections with Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Surette MG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Autoinducer-2; AI-2; antibiotic; antibacterial; dermatological; vulnerary; pheromone; agr system; accessory gene regulator; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide-mediated quorum sensing inhibitor peptide cyclo-XII.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB 3; Length 9;
Pred. No. 1.7e+06;
Mismatches 2; Indels
                                                                                                                                                                                                                                                        Beavis
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(QUOR-) QUOREX PHARM INC.
(UYTB-) UNIV TECHNOLOGIES INT INC.
                                                                                                                                                                                                                                                    Muir TW, Mayville P, Novick RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB07160 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                        Example; Page 22; 37pp; English.
                                                                                                                                                                      98US-00103438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.2%;
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                                                                                                                                                                                                     (UYRQ ) UNIV ROCKEFELLER.
(UYNY ) UNIV NEW YORK STATE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S)
                                   Staphylococcus aureus.
                                                                                                                                                                                                                                                                                    WPI; 2000-147202/13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GANAXSSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GUNAASSLF
     virulence factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200185664-A2
                                                                                                                                     24-JUN-1999;
                                                                     WO9967286-A2
                                                                                                                                                                      24-JUN-1998;
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                                                                                                   29-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bassler BL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB07160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the Staphylococcus aureus AgrDII derived peptide. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New cyclic peptides for treating infections with Staphylococcus aureus.
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                 Staphylococcus aureus infection; AgrD; agr response; treatment; virulence factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus infection; treatment; AgrD; agr response;
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 Indels
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Pred. No. 1.7e+06;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                 Staphylococcus aureus AgrDII derived peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus AgrDII derived peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beavis R;
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mayville P, Novick RP,
                                                                                                                                            AAY67860 standard; peptide; 9 AA.
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(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                 (first entry)
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Best Local Similarity 77.0
Best Local 7; Conservative
Conservative
                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus.
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                               GANAXSSLF
                                                              GANAXSSLF
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Muir TW,

25-APR-2000

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AAY67859

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AAY67859

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24-JUN-1999;
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08-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                              infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM51004;
         Muir IW,
                                                                  subject.
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                                                                                            antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis. Synergistic antibiotic compositions compositions compositions are also provided. Methods using such Al-2 analogues are useful for treating pathogen-associated disease states. The compounds and antibiotic compositions can be used to inhibit bacterial cell growth and/or biofilm formation on a medical device, particularly for promoting growth of skin graft replacements used in the treatment of burns and ulcers. They may also be used to aid wound repair, and to inhibit bacterial cell growth and buffilm formation in or on products or devices used for personal hygiene. The present sequence represents a inhibitor of periode-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "note linked to residue 9 to form cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "note linked to residue 5 to form cyclic peptide"
                           Use of autoinducer-2 agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis, also antibiotic compositions.
                                                                                                                                                                                                                                                                  Gaps
                                                                                      The invention relates to the use of autoinducer-2 (AI-2) agonists
                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic; antibacterial; infection; therapy; cyclic.
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                                                                                                                                                                                                                                            Score 34; DB 5; Length 9;
Pred. No. 1.7e+06;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Protected peptide used in cyclic peptide production.
                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Ser(Bzl)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Ser (tBu) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Ser(Bzl)"
                                                                                                                                                                                                                                                                                                                                                       AAM50907 standard; peptide; 9 AA
                                                                                                                                                                                                                                            87.2%;
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(UYNY ) UNIV NEW YORK STATE.
                                                                    Disclosure; Page 33; 134pp;
                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                     1 GANAXSSLF
                                                                                                                                                                                                                                                                                                 GVNASSSLF
                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                            Sequence 9 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                           AAM50907;
                                                                                                                                                                                                                                                                                                                                     RESULT 7
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The present sequence is that of a protected peptide used in an example of the preparation of novel synthetic cyclic peptides of the invention (see AAMS0899-906). The peptide corresponds to the Staphylococcus aureus agreeme with a CyS5 to Ser mutation (lactone). It was synthesised on a Wang-reain using an Froc N-alpha protection strategy. Following con a mang-reain using an Froc N-alpha protection strategy. Following confaintsole. We treatment with a trifluoroacetic acid:anisole. Water mixture (90:5:5) for 4 hr. The partially protected peptide acatoxylates were then dissolved in DMF and treated with complete after 2 hr. The remaining protecting groups were then removed by treatment with HF and the peptide purified by HPLC. The cyclic peptide is capable of inhibiting the agr response of Staphylococcus aureus. The thiololatone structure within native AgrD peptides is required for activation of this response. Replacement of the thiol ester component of the cyclic ring structure within alatone (as in the present asse) or a lactam can destroy agr response activating activity while preserving and canadian inhibitory activity. The cyclic peptides are useful for changed in the freezent of S. aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "note linked to residue 9 to form cyclic peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                         Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in
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   Beavis R,
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   Novick RP,
                                                                                                                                                                                                                                                              Disclosure; Col 14; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM51004 standard; peptide; 9 AA.
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77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AgrD2 lactone cyclic peptide.
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Best Local Similarity 7//07
7/ Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy; lactone; cyclic
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   Mayville P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus
                                                                  WPI; 2002-170774/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVNASSSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GANAXSSLF
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Mayville P, Novick RP,
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                                                                                                                                                                                                                                                                            AAM51003 standard; peptide; 9 AA.
                                                                       Example 1; Col 9; 18pp; English
                                                                                                                                                                                                                                                                                                                 AgrD2 linear free acid peptide.
                                                                                                                                                                                                                                                                                                                                                                                          99US-00339511
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     ) UNIV ROCKEFELLER.
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(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                     (first entry)
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus.
Synthetic.
                                                                                                                                                                                                                                   1 GANAXSSLF 9
                                                                                                                                                                                                                                              1 GVNASSSLF 9
                                   WPI; 2002-170774/22.
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                                                                                                                                                                                               Sequence 9 AA;
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                       Muir TW,
                                                                                                                                                                                                                                                                                        AAM51003;
                                                           subject.
                                                                                                                                                                                                                                                                                                                                    therapy.
     (UYRQ
(UYNY
                                                                                                                                                                                                                                                                 RESULT 9
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The present sequence is that of a novel synthetic AgrD2 linear free acid peptide. The peptide is derived from the cyclic AgrD2 peptide of Staphylosocous aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured so aureus strains containing a beta-lactamase reporter gene fused to the agrs promoter. This allowed activation or inhibition of the agr response to be monitored spectrophotometrically. Unlike an AgrD2 thiololactone cyclic peptide (see AAM51001), the present peptide was unable to either activate or inhibit the agr response, even when added to cultured cells at un concentrations. The invention provides claimed cyclic peptides are useful for bacterial interference, especially for the peptides are useful for bacterial interference, especially for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
                    Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in a subject.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.2%; Score 34; DB 5; Length 9; 77.9%; Pred. No. 1.7e+06; Live 0; Mismatches 2; Indels
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9
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                                                                                                    Example 1; Col 9; 18pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AgrD2 linear thioester peptide.
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(UYNY ) UNIV NEW YORK STATE.
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus. Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
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ID AAM5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of a novel synthetic AgrD2 lactone cyclic peptide in which residue 5 of the peptide is linked to residue 9 via a lactone bond. The peptide is linked to residue 9 via a lactone bond. The peptide is derived from an AgrD2 peptide 6 staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide. Expaphylococcus aureus strains responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agricultured specifically. The lactone AgrD2 peptide inhibited the agr response of group I S. aureus strains without activating them a response of group I S. aureus strains without provides claimed cyclic peptides (see AAMS0899-906 and AAMS0899) and methods for preparing them especially peptides where the cyclic bond is a linterference, especially for the treatment of S. aureus infection.

(Updated on 07-NUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                            Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87.2%; Score 34; DB 5; Length 9; 77.8%; Pred. No. 1.7e+06; tive 0; Mismatches 2; Indels
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                                                                              Beavis R,
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Gaps

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The present sequence is that of a novel synthetic AgrD2 linear thioester peptide. The peptide is derived from the cyclic AgrD2 peptide of Stapplylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agr promoter. This allowed activation or inhibition of the agr response to be monitored spectropherometrically. Unlike an AgrD2 thiololactone cyclic peptide (see AAM51001), the present peptide was unable to either activate or inhibit the agr response, even when added to cultured cells at um concentrations. The invention provides claimed cyclic peptides are useful for bacterial interference, especially for the cyclic peptides are useful for bacterial interference, especially for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New cyclic peptides for treating infections with Staphylococcus aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus infection; cyclic peptide; AgrD; agr response; virulence factor; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 5; Length y;
Pred, No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aureus peptide #1 used for bacterial interference.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY67851 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; Page 26; 37pp; English.
Example 1; Col 9; 18pp; English
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(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.2%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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Best Local Similarity
7; Conserve
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LID AAY67851

LID AAY67851

AAY67851
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activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New cyclic peptides for treating infections with Staphylococcus aureus.
                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus infection; AgrD; agr response; treatment;
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                                                                                                                                                                                                                                                                                                          Staphylococcus aureus AgrDII derived peptide sequence.
                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beavis
                                                                                Score 33; DB 3; I
Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 3; I
Pred. No. 1.7e+06;
0; Mismatches 1;
                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                84.68;
88.98;
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(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                  (first entry)
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Best Local Similarity 88.9
Matches 8, Conservative
                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus
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                                                                   Query Match
Best Local Similarity
Fee 8, Conserve
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                                                                                                                                     1 GANAXSSLF
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                                                      Seguence 9 AA;
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ID AAY
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The present sequence is that of a novel synthetic AgrD2 lactam cyclic peptide in which residue 5 of the peptide is linked to residue 9 via a car datem bond. The peptide is derived from an AgrD2 peptide of Jactam bond. The peptide is derived from an AgrD2 peptide of Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other controls proteins responsable for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured of S. aureus strains containing a beta-lactamase reporter gene fused to the agr spromoter. This allowed activation or inhibition of the agr response in group I S. aureus strains and did not activate the agr response in group I S. aureus strains and did not continued for provides claimed cyclic peptides (see AAMS0899-906 and AAMS0899) and continued for preparing them, especially where the cyclic boptides continued for preparing them, especially where the cyclic boptides can use useful for bacterial interference, especially for the treatment of S. aureus infection.

C. Updated on 07-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                            'note= "note linked to residue 9 to form cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                  /note= "note linked to residue 5 to form cyclic peptide"
                                                                                                                        response; inhibitor; antibiotic; antibacterial; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in a subject.
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88.9%; Pred. No. 1.7e+06;
ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beavis R,
                                                                                                                                                                                                                                                                                                                                       'note= "any amino acid"
                                                                                                                                                                                                                                              Location/Qualifiers
5
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AAMSO908
ID AAMSO908 standard; peptide; 9 AA.
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(UYNY ) UNIV NEW YORK STATE.
                                                                                 AgrD2 lactam cyclic peptide
                  (revised)
(first entry)
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                                                                                                                                                                                   Staphylococcus aureus.
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Matches 8; Conserv
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Misc-difference
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                                                                                                                        AgrD2; agr responderapy; cyclic
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               07-AUG-2003
08-MAY-2002
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                                                                                                                                                                                                              Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to the use of autoinducer-2 (AI-2) agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis. Synergistic antibiotic compositions comprising inhibitors of the quorum-sensing pathway of a microorganism are also provided. Methods using such AI-2 analogues are useful for treating pathogen-associated disease states. The compounds and antibiotic compositions can be used to inhibit bacterial cell growth and/or bidfilm formation on a medical device, particularly for promoting growth of skin graft replacements used in the treatment of burns and ulcers. They may also be used to aid wound repair, and to inhibit bacterial cell growth and bygiene. The present sequence represents a inhibitor of personal hygiene. The present sequence represents a inhibitor of peptide-mediated quorum sensing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of autoinducer-2 agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis, also antibiotic compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Surette MG;
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                                                                                                                                                                                                                              Autoinducer-2; AI-2; antibiotic, antibacterial, dermatological, vulnerary; pheromone, agr system; accessory gene regulator, cyclic.
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                                                                                                                                                                                        Peptide-mediated quorum sensing inhibitor peptide cyclo-XIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stein J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                  /note= "diaminoprprionic acid residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shokat K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB 5; L
Pred. No. 1.7e+06;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schauder S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 33; 134pp; English.
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYPR-) UNIV PRINCETON,
(QUOR-) QUOREX PHARM INC.
(UYTE-) UNIV TECHNOLOGIES INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM51005 standard; peptide; 9 AA.
                                                           ABB07161 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-2001; 2001WO-US015221.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAY-2000; 2000US-0203000P.
                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bassler BL, Dammel CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-075235/10.
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                                                                                                                                                                                                                                                                                                                                            Key
Modified-site
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15-NOV-2001

Synthetic.

ABB07161;

RESULT 13 **ABB0716**1 ö

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AAM51005

RESULT 14
AAM51005
ID AAM51
XX
AC AAM51

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The present sequence is that of a protected peptide used in an example of the preparation of novel synthetic cyclic peptides of the invention (see AANSOB99-906). The peptide corresponds to the Staphylococcus aureus AANSOB99-906. The peptide corresponds to the Staphylococcus aureus aprent in was synthesised on a Wang-reain using an Func N-alpha protection strategy. Following chain assembly, the peptide was cleaved from the support and the Dr-5 residue deprotected by treatment with a trifluoroacetic acid-anisola-water mixture (90:5:5) for 4 hr. The created with PyBOP. Cyclization was complete after 2 hr. The reated with PyBOP. Cyclization was complete after 2 hr. The remaining protecting groups were removed by treatment with HF and the peptide purified by HPLC. The cyclic peptide is capable of inhibiting the capture of Staphylococcus aureus. The thiololactone structure within native AgrD peptides is required for activation of this response. Replacement of the thiol ester component of the cyclic ring structure with a lactam (as in the present case) or a lactone can destroy agr response activating activity while preserving and enhancing inhibitory activity. The cyclic peptides are useful for bacterial interference,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novick RP, Beavis R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Col 14; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-00339511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0090402P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYRQ ) UNIV ROCKEFELLER.
(UYNY ) UNIV NEW YORK STATE.
                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muir TW, Mayville P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-170774/22.
                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                              Key
Modified-site
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                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                        Modified-site
                                         08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JUN-1998;
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                                                                                                                                                 Synthetic
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Query Match 84.6%; Score 33; DB 5; Length 9; Best Local Similarity 88.9%; Pred. No. 1.7e+06; Matches 8; Conservative 0; Mismatches 1; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "note linked to residue 9 to form cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "note linked to residue 5 to form cyclic peptide"
                                                                                                                                                                                                 Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic; antibiotic; antibacterial; infection; therapy; cyclic.
                                                                                                                                            Protected peptide used in cyclic peptide production.
                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Ser(Bzl)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "Ser(Bzl)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'label= Dpr(Boc)
                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Z-Gly"
                            AAM50908;
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1 GVNAXSSLF
g
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1 GANAXSSLF

Search. completed: October 26, 2004, 15:59:40 Job time: 44.75 secs

153, App 38573, A 269654, Ap 269654, A 45245, A 1286, Ap 47013, A 67013, A 68077, A 68077, A 68077, A 6111286, A 111286, A 111286, A

Sequence Sequence Sequence Sequence Sequence Sequence

2, Appli 3, Appli 497, App

Sequence Sequence Sequence

Sequence Sequence

Sequence Sequence Sequence

Sequence

Sequence 492, App Sequence 174213,

303, Âpp 190059, 151008, 59048, A

Sequence

Sequence Sequence

Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence

1

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JOSEPHONE 2, APPLICATION US/10032950

PUBLICATION NO. US20020077453A1

GENERAL INFORMATION:

APPLICANT: Mayville, Patricia

APPLICANT: Mayville, Patricia

APPLICANT: Mo. US20020077453A1ick, Richard P.

TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL

TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL

TITLE OF INVENTION: UNDER: US/10/032,950

CURRENT APPLICATION NUMBER: 60/090,402

PRIOR APPLICATION NUMBER: 60/090,402

PRIOR FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PATENTIN VOY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide NAME/KEY: VARIANT LOCATION: (5) OTHER INFORMATION: Xaa represents any amino acid at this position.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
94.9%; Score 37; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels
US-10-368-687-30

US-10-368-687-32

US-10-368-687-28

US-10-368-687-28

US-10-368-687-28

US-10-108-605-303

US-10-465-91-10059

US-10-445-599-190059

US-10-767-701-59048

US-10-787-701-59048

US-10-787-701-5907

US-10-787-701-5007

US-10-425-114-65481

US-10-437-963-164712

US-10-437-963-164712

US-10-437-963-164712

US-10-437-963-164712
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US-10-416-249-492
US-10-424-599-174213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
   1 GANAXSSLF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS-10-032-950-2
   SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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Sequence 1, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 72514, A
Sequence 120758,
Sequence 111282,
Sequence 5, Appli
Sequence 5, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                             October 26, 2004, 15:54:00 ; Search time 31.5 Seconds (without alignments) 92.502 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1
Sequence 1
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/NS07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_MBW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/NS06_NBW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_NBW_PUB.pep:*

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7: /cgn2_6/ptodata/2/pubpaa/NS08_PUBCOMB.pep:*

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9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

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11: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09_NBW_PUB.pep:*

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18: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

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10: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-032-950-1
US-10-201-444-6
US-10-201-444-6
US-10-282-122A-4889
US-10-437-963-120758
US-10-437-963-111282
US-10-032-950-5
US-10-032-950-6
US-10-425-914-47226
US-10-424-599-161195
                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                             1364641 seqs, 323758627 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                               protein search, using sw model
                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                             US-10-032-950-2
39
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                                                                                                                                                                                                            1 GANAXSSLF 9
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Match 1
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                                                                               OM protein
                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                             Searched:
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                                                                                                                Run on:
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FEATURE:
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US-10-201-444-3
US-10-201-444-3
Sequence 3, Application US/10201444
Publication No. US20030078378A1
GENERAL INFORMATION:
APPLICANT: New York University Medical Center
APPLICANT: New York University Medical Center
TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
FILE REFERENCE: 63753/7
CURRENT APPLICATION NUMBER: US/02-07-23
PRIOR APPLICATION NUMBER: US/08/861,476
PRIOR APPLICATION NUMBER: US/08/861,476
PRIOR APPLICATION NUMBER: US/08/861,476
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
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                                                                                                                                                  ## Sequence 1, Application US/10032950
| Publication No. US200200077453A1
| GENERAL INFORMATION:
| APPLICANT: Mayville, Parricia |
| APPLICANT: Mayville, Parricia |
| APPLICANT: Mayville, Parricia |
| APPLICANT: Beavis, Ronald |
| APPLICANT: No. WORLE, STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL |
| TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL |
| TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL |
| FILE REFERENCE: 600-1-231M |
| CURRENT APPLICATION NUMBER: 60/090,402 |
| PRIOR APPLICATION NUMBER: 60/090,402 |
| PRIOR FILING DATE: 1998-06-24 |
| NUMBER OF SEQ ID NOS: 8 |
| SOFTWARE: PATENTIN Ver: 2.0 |
| SEQ ID NO 1 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Synthetic COTHER INFORMATION: peptide
NAME/KEY: VARIANT
LOCATION: (5)
OTHER INFORMATION: Xaa represents any amino acid at this position. US-10-032-950-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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US-10-201-444-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 88.9
Matches 8; Conservative
1 GANAXSSLF 9
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                                                                                                         RESULT 2
US-10-032-950-1
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GVNACSSLF 9

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Sequence 72514, Application US/10425114

Sequence 72514, Application US/10425114

Publication No. US20040034888A1

SEMENTAL INFORMATION

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Paparicant: Norgemi

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFREENCE: 32-21(5313)B

CURRENT APPLICANT: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 72514

LENGTH: 340
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ASQUENCE 6, Application US/10201444

Sequence 6, Application US/10201444

PUBLICANT: New York University Medical Center

APPLICANT: New York University Medical Center

ITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS

FILE REFERENCE: 6375/7

CURRENT APPLICATION NUMBER: US/10/201,444

CURRENT FILING DATE: 1207-07-23

PRIOR APPLICATION NUMBER: US/08/861,476

PRIOR PLING DATE: 1997-05-22

NUMBER OF SEQ ID NOS: 8

SSOFWARES: Patentin version 3.0

LENGTH: 47
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Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 82.1%; Score 32; DB 14; Length 47; Best Local Similarity 77.8%; Pred. No. 9; Matches 7; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: Clone ID: UC-ZMFLMO17229E06_FLI.pep
US-10-425-114-72514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-282-122A-48898
; Sequence 48898, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Haselbeck, Robert
; APPLICANT: Oblisen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-201-444-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 GVNACSSLF 32
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-10-425-114-72514
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APPLICANT: LA ROSA, Thomas J.
APPLICANT: LA ROSA, Thomas J.
APPLICANT: LA ROSA, Thua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)
FULE REFERENCE: 38-21(53221)
CURRENT APPLICATION NUMBER: US/10/437,963
NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                          Gaps
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
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APPLICANT: Mayville, Patricia
APPLICANT: Mayville, Patricia
APPLICANT: Mayville, Patricia
APPLICANT: Beavis, Ronald
APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
FILE REPERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/10/032,950
GURRENT FILING DATE: 2001-12-27
PRIOR FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.5%; Score 31; DB 16; Length 1804; 66.7%; Pred. No. 7.3e+02; Live 2; Mismatches 1; Indels (
                                                                                             Length 1203;
                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT4530_15275C.1.pep
US-10-437-963-111282
, OTHER INFORMATION: Clone ID: PAT_MRT4530_2384C.1.pep
US-10-437-963-120758
                                                                                          Score 31; DB 16;
Pred. No. 4.7e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 111282, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 5, Application US/10032950
; Publication No. US20020077453A1
; GENERAL INFORMATION:
                                                                                          79.5%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 8 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 5 LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.77
                                                                                   Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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712 GANALATLF 720
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LENGTH: 1804
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Publication No. US20040123343A1

Sequence 120758, Application US/10437963

Publication No. US20040123343A1

GENERAL INPORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Vinua

APPLICANT: Cao, Yongwei

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT FILING DATE: 2003-05-14

SEQ ID NO 120758

SEQ ID NO 120758
                                                                                                   APPLICANT: Carr, Garnt
APPLICANT: Forsyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PRILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/265,308
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-16
PRIOR PRILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-06
PRIOR PRI
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Pred. No. 1.9e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.9e+02;
~hes 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Bacteroides fragilis US-10-282-122A-48898
                                   Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.7
Page 6; Conservative
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ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -10-437-963-120758
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76.9%;
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Best Local Similarity 66.7
Matches 6; Conservative
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ORGANISM: Glycine max
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Best Local Similarity
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US-10-424-599-161196
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US-10-425-114-47226

Squence 47226, Application US/10425114

Publication No. US2040034888A1

SQUENCE 47226, Application US/10425114

Publication No. US2040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Screen, Steven E

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)8

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 47226
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Fublication No. US20020077453A1

GENERAL INFORMATION:
APPLICANT: Maryville, Patricia
APPLICANT: Mayville, Patricia
APPLICANT: Beavis, Ronald
APPLICANT: Deavis, Ronald
APPLICANT: Deavis, Ronald
APPLICANT: UN. US20020077453A1ick, Richard P.
APPLICANT: No. US20020077453A1ick, Richard P.
APPLICANT: Deavis, Ronald
APPLICANT: J. Guangyons
TITLE OF INVENTION: INTERPERENCE
TITLE OF INVENTION: INTERPERENCE
TITLE OF INVENTION: UNBER: US/10/032.950
CURRENT FILING DATE: 1998-06-24
FRICR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 6
TENGRAD APPLICATION OF 2.0
; OTHER INFORMATION: peptide
; NAME/KEY: VARIANT
; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide NAME/KEY: VARIANT LOCATION: (5) OTHER INFORMATION: Xaa represents any amino acid at this position.
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                                                                                                                                76.9%; Score 30; DB 13; Length 9; 77.8%; Pred. No. 1.2e+06; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.9%; Score 30; DB 13; Length 9; 77.8%; Pred. No. 1.2e+06; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                              Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 76.9
Best Local Similarity 77.8
Matches 7; Conservative
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1 GVNAXSALF 9
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US-10-032-950-6
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APPLICANT: Lower thomas J
APPLICANT: Acvaltc David K
APPLICANT: Acvaltc David K
APPLICANT: Show Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223)8
CURRENT APPLICANION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 288684
ENGINE OF SEQ ID NOS: 288684
LENGTH: 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16195; Application US/10424599
Sequence 16195; Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEG ID NOS: 285684
SEQ ID NO 161195
LENGTH: 247
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                                                                                                                                                                                                     Length 121;
                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: Clone ID: PAT_MRT3847_116578C.1.pep
US-10-424-599-161196
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US-10-424-599-161195
; LENGTH: 121
; TYPE: PRT
; CRGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3115-032-H10_FLI.pep
US-10-425-114-47226
                                                                                                                                                                                                  76.9%; Score 30; DB 15;
66.7%; Pred. No. 69;
tive 2; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 161196, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
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Search completed: October 26, 2004, 16:10:10 Job time : 32.5 secs

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US-10-366-687-30

i Sequence 30, Application US/10368687

i Publication No. US2003162713A1

Sequence 30, Application US/10368687

i Publication No. US2003162713A1

APPLICANT: Turner, Alex

APPLICANT: Priedrich, Glenn

APPLICANT: Friedrich, Glenn

APPLICANT: Sands, Arthur T.

ITLE OF INVENTION: No. US20030162713A1e1 Human Transporter Proteins

FILE REFERENCE: 8353-641-999

CURRENT FILING DATE: 2003-02-14

PRIOR FILING DATE: 2000-04-21

NUMBER OF SEQ ID NOS: 32

SOFTWARER PARSERS PARSERS US/09/556,916

NUMBER OF SEQ ID NOS: 32

SOFTWARER PARSERS PARSERS OF FOR Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-18-6-84-92

US-10-18-98-97-92

US-10-18-98-97-92

Publication No. US2030162713A1

GENERAL INFORMATION:

APPLICANT: Zambrowicz, Brian

APPLICANT: Neblas

APPLICANT: Neblas

APPLICANT: Neblas

APPLICANT: Sands, Arthur T.

TILE OF INVENTYON: No. US2030162713A1e1 Human Transporter Proteins

FILE REFRENCE: 8535-041-999

CURRENT APPLICATION NUMBER: US/10/368,687

CURRENT APPLICATION NUMBER: US/09/556,916

PRIOR APPLICATION NUMBER: US/09/556,916

PRIOR PILING DATE: 2000-04-21

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSEQ for Windows Version 3.0

SOFTWARE: FastSEQ for Windows Version 3.0

CORGANISM: Homo sapiens

US-10-368-687-32
  Gaps
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  Indels
1; Mismatches
6; Conservative
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150 GASALSSMF 158
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                                                                                  55 GANATSSI 62
                                       1 GANAXSSL 8
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US-10-368-687-32
Matches
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: October 26, 2004, 15:46:55; Search time 8.73529 Seconds

Without alignments)

Perfect score: 39
Sequence: 1 GANAXSSLF 9
Sequence: 1 GANAXSSLF 9
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 00000000

Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%
Listing first 45 summaries

Database: PIR 79:*
1: Pirl:*
3: Pirl:*
4: Pirl:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8CT.	transcription fact	lysosomal membrane	P2B/LAMP-1 precurs	120K lysosomal mem	AgrD protein [impo	-cyt	peptidase (M3 fami	hypothetical prote	hypothetical prote	multidrug resistan	conserved hypothet	probable membrane	protein C18B10.10	ferrichrome ABC tr	receptor-protein k			probable flavoprot	n.	probable outer mem	Similar to Cytochr	probable ubiquitin	hypothetical prote	hypothetical prote	Ł	hypothetical prote	hypothetical prote		hypothetical 24.8
ı																													
_	S58439	A28067	A60534	A30200	C89995	ZPBOC2	F81313	S76294	T04998	T06165	F83144	H84428	C89103	C69812	T45786	B64725	E85485	E90634	B85757	A99862	D86306	C84549	S74291	T32930	H83357	T16158	B87290	80	D65105
DB	2	~	N	N	N	Н	N	~	~	7	7	~	~	Н	7	~	7	7	7	~	N	~	N	N	~	N	N	~	(7)
Length	269	œ	405	0	47	453	573	340	536	1232	213	250	291	333	895	313	313	313	342	457	476	551	870	1435	12	71	186	211	226
% Query Match	84.6	84.6	4.	84.6	2	ä	82.1	φ.	φ.	φ.	è.		œ		76.9	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4			71.8	71.8
Score		33				32	32	31	31	31	30	30	30	30	30	29	29	29	29	29	29	29	29	29	29	28	28	28	28
Result No.	-	7	m	4	Ŋ	ø	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	20

A; Molecule type: mRNA

hypothetical prote hypothetical prote		probable sugar-bin conserved hypothet	indoleamine-pyrrol	probable chitinase	probable DNA-bindi	hypothetical prote	hypothetical prote	hypothetical prote	SEC24 protein - ye	DNA-directed DNA p	coatomer complex a	probable integral
D85978 A98133	S64931 A84187	AD0105 B71307	S57097	T24127	G96713	T05210	B85398	T41402	S48463	A81343	T02146	A37361
01 01	N N	0 0	N	N	N	N	N	N	N	N	N	~
226	344	420 429	453	453	486	513	546	715	926	1200	1216	1938
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71.7	71	71.7	71.	71.	71	71.	71.	7	71	71.	71	71
2 8 8 8	7 8 7 8 8 8	7 7 8 8 8 7	28	28	28	28	28	28	28	28	28	28
30 31	9 9 9	34 35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

S58439
NATICENTATE NAMES: WOLVAN KNOCKEG-related procein; nomeotic procein Anx C.seccise: Gallus callus (Chicken)
C.Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Aug-2004
C.Accession: S58439; S58440
KKYAN, A.K.; IBJada, m.L.; May, D.L.; Dudgova, m.; Deeley, K.C. submitted to the EMBI Data Tibrary, Abril 1995
A, Description: Isolation and characterization of the chicken homeodomain protein AKR.
A;kererence number: 55843y A;Accession: S58439
A; Molecule type: mRNA
A,Residues: 1-269 <rva></rva>
A/CTOSS-TERETERGES: UNI-MYCLIQUESE); EMBLIOLZ-33; N. LIDUGSS-7681; F.LIDN:AAAR355/11; F.LUGSS/ R. Povan. A. K. + Tejada, M. T. + Mav. D. T. + Dubacva, M. + Deelev. R.G.
Nucleic Acids Res. 23, 3252-2259, 1995
A,Title: Isolation and characterization of the chicken homeodomain protein AKR.
A; Reference number: SSB440; MULD:95396587; PMLD:766/LUZ
A;Actatus: nucleic acid sequence not shown A.Status: nucleic acid sequence
A; Molecule type: mRNA
A, Residues: 35-94 < RYF>
A;Cross-relevences: EMBL:UZ5353
on: negative regulator of apoVLDLII (major egg yolk apolipoprotein)
early embryogenesis
C;Superfamily: homeobox homology
C.Neywords: DNA Dinding) Homeobox; Hudleus; Lighborlin regulation F/36-95/Domain: homeobox homology <hox></hox>
84.6%; Score 33;
Similarity 77.8%; Pred. No. 3.9; 7; Conservative 0; Mismatches
Db 222 GANAQSGLF 230
KESULI 2 A28067
lysosomal membrane glycoprotein LAMP-1 - mouse
C,Species: Mus musculus (house mouse) C.Date: 30-Sen-1989 #sequence revision 30-Sen-1989 #text change 09-Jul-2004
R;Chen, J.W.; Cha, Y.; Yuksel, K.U.; Gracy, R.W.; August, J.T. T Biol Cham 263 8754-8758 1988
o this community of a community of a cDNA clone encoding lysosomal membrane glycoprot A; fitle: Isolation and sequencing of a cDNA clone encoding lysosomal membrane glycoprot
A; Reference number: A28067; MUID:88243732; PMID:3379044
A; Accession: A2806/

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Gaps

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Algocesule type: mRNA
A/Rocesule type: mature protein, was confir
B/Cocco, T.; Lorusso, M.; Sardanelli, A.M.; Minuto, M.; Ronchi, S.; Tedeschi, G.; Papa,
Bur. J. Blochem. 195, 731-734, 1991
Bur. J. Blochem. 195, 731-734, 1991
A/Rocesule type: Brother type: Drocesule type: Drocesule type: Drocesule type: Drocesule type: Drocesule type: protein
A/Rocesule type: protein
A/Rocesule type: protein
A/Rocesule type: protein
A/Rocesule type: procesule matrix: mitochondrial processing peptidase alpha chain
C/Superfamily: mitochondrial processing matrix: mitochondrion; oxidative phosphorylation; C/Superfamily: mitochondrial matrix: mitochondrion; experimental
F/1-4/Domain: transit peptide (mitochondrion) #status protein II #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:033586; GB:BA000018; PID:g13701831; PIDN:BAB43124.1; GSPDB:GA;Experimental source: strain N315
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Species: Bos primigenius taurus (cattle)
C.Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C.Accession: S16221, S14033
Eur. J. Blochem. 199, 123-131, 1991
A;Tile: Core I protein of bovine ubiquinol-cytochrome-c reductase; an additional member re of the proteins.
A;Reference number: S16220; MUID:91293112; PMID:1712295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: C89995
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Cai, M.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, B.; Shiba, T.; Hatori, M.; Ogaswara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89788; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ubiquinol-cytochrome-c reductase (EC 1.10,2.2) core protein II precursor - bovine
                                                                                                                                                                                                                                                                                                                                                                                                     AgrD protein [imported] - Staphylococcus aureus (strain N315)
C,Species: Staphylococcus aureus
C,Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
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2,
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llarity 77.8%; Pred. No. 1.1;
Conservative 0; Mismatches
    0; Mismatches
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Matches 6; Conservative
    7; Conservative
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Best Local Similarity
Matches 7; Conserv
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PSTS / LAW - I precursor - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Accession: A60534
R; Heffernan, M.; Yousefi, S.; Dennis, J.W.
Cancer Res. 49, 6077-6084, 1989
A; Title: Molecular characterization of P2B/LAMP-1, a major protein target of a metastasi A; Accession: A60534
A; MuD: 90002989; PMID: 2676155
A; Accession: A60534
A; MuD: 90002989; PMID: 2676155
A; Accession: A60534
A; MuD: 90002989; PMID: 2676155
A; Accession: A60534
A; Multiple: Multiple
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NyAlternate names: sialoglycoprotein
NyAlternate names: sialoglycoprotein
NyAlternate names: sialoglycoprotein
NyAlternate names: sialoglycoprotein
CySpecies 18-0ct-1898 #seguence [Norway rat]
CyBaccession: A30200; S0331
CyAccession: A30200; S0331
CyAccession: A30200; S0331
Proc. Natl. Acad. Sci. U.S.A. 85, 7577-7581, 1988
A;Title: Derived protein sequence, oligosaccharides, and membrane insertion of the 120-k
A;Reference number: A30200; MUID:89017240; PMID:3174652
A;Accession: A30200.
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A; Residues: 1-407 <h0N>
A; Cross-references: UNTROT: P14562; EMBL: J03672
A; Cross-references: UNTROT: P14562; EMBL: J03672
A; Note: the authors translated the codon GGG for residue 15 as Val
R; Himeno, M.; Noguchi, Y.; Sasaki, H.; Tanaka, Y.; Furuno, K.; Kono, A.; Sakaki, Y.; Kat
FEBS Lett. 244, 351-356, 1989
A; Title: Isolation and sequencing of a cDNA clone encoding 107 kDa sialoglycoprotein in
A; Reference number: S03331; MUD: 89153580; PMID: 2920835
A;Residues: 1-382 <CHE>
A;Cross-references: UNIPROT:P11438; GB:J03881; NID:g198706; PIDN:AAA39411.1; PID:g293692
A;Cross-references: UNIPROT:P11438; GB:J03881; NID:g198706; PIDN:AAA39411.1; PID:g293692
A;Orce: the authors translated the codon ATT for residue 1 as Leu and CCG for residue 2
C;Superfamily: lysosome-associated membrane protein
C;Keywords: glycoprotein; membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: mRNA
A,Residues: 22-407 - HHM>
A,Gross-references: EMBL:X14765; NID:956577; PIDN:CAA32873.1; PID:956578
A,Note: part of this sequence, including the amino end of the mature protein, was confix
C,Superfamily: lysosome-associated membrane protein
C,Keywords: glycoprotein; membrane protein
F;22-407/Product: lysosomal membrane glycoprotein, 107K #status experimental <MAT>
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                                                                                                                                                                                                                                                                        84.6%; Score 33; DB 2; Length 382; 77.8%; Pred. No. 5.6; ive 0; Mismatches 2; Indels
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Pred. No. 6;
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Best Local Similarity 77.0
Lac 7; Conservative
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity

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A,Status: preliminary
A,Molecule type: DNA
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Matches
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peptidase (M3 family) Cj1099 [imported] - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: P81313
R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C:W.; Outlet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: P81313
A;Status: preliminary
A;Accession: P81313
A;Status: preliminary
A;Residues: 1-573 cPAR>
A;Coss-references: UNIPROT:Q9PNJ5; GB:AL139077; GB:AL11168; NID:g6968444; PIDN:CAB7335
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics: Cj1099
C;Superfamily: oligoendopeptidase F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cispecies: Synechocystis sp.

A;Variety: PCC 6803

A;Variety: PCC 6803

C;Accession: S76294

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

B)NA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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A.Residues: 1-340 «KAN»
A.Cross-references: UNIPROT.Q55632; EMBL.D64000; GB.AB001339; NID.g1001484; PIDN.BAA1014
A.Cross-references: UNIPROT.Q55632; EMBL.D64000; GB.AB001339; NID.g1001484; PIDN.BAA1014
C.Genetics:
A.Start codon: GTG
C.Superfamily: hypothetical protein sll0462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein T16L1.300 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004 C;Accession: T04998 R;Bevan, M.; Obermaier, B.; Deutschenbaur, S.; Piravandi, E.; Hoheisel, J.; Mewes, H.W. submitted to the Protein Sequence Database, November 1998 A;Reference number: Z15393
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A,Accession: S76294
A,Status: nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Length 340;
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Pred. No. 15;
0; Mismatches
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Best Local Similarity 77.8%;
Matches 7; Conservative
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ilarity 87.5%;
Conservative
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Best Local Similarity
Matches 7; Conserv
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Toffice Toffice Teststance protein 1 homolog - barley
C,Species: Hordeum vulgare (barley)
C,Species: Hordeum vulgare (barley)
C,Accession: Toffics
R,Cocession: Toffics
R,Davies, T. G.E.; Theodoulou, F.L.; Hallahan, D.L.; Forde, B.G.
Gene 199, 195-202, 1997
A,Fitle: Cloning and characterization of a novel P-glycoprotein homologue from barley.
A,Reference number: 215500; MUID:98019088; PMID:9358056
A,Accession: Tofics
A,Residues: 1-1232 cDAV
A,Cross-references: UNIRROT:023998; EMBL:Y10099; NID:92292906; PIDN:CAA71179.1; PID:922
A,Resperimental source: cv. Maris Mink
C;Superfamily: multidrug resistance protein; ATP-binding cassette homology
F;381-575/Domain: ATP-binding cassette homology cABC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conserved hypothetical protein PA4017 [imported] - Pseudomonas aeruginosa (strain PA01) C; Species: Pseudomonas aeruginosa C; Species: Pseudomonas aeruginosa (cjate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004 C; Accession: F83144 R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; B adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim., Lory, S.; Olson, M.V.

J. Lory, S.; Olson, M.V.

J. Lory, S.; Olson, M.V.

J. Artitle: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path A; Reference number: A82950; MUID:20437337; PMID:10984043
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A;Cross-references: UNIPROT:O9HX10; GB:AE004818; GB:AE004091; NID:g9950200; PIDN:AAG074
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA4017
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Pest Local Similarity 66.7%; Pred. No. 58;
Matches 6; Conservative 2; Mismatches 1; Indels
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A;Molecule type: DNA
A;Residues: 1-536 <BEV>
A;Cross-references: UNIPROT:081897; EMBL:AL031394
A;Cross-references: UNIPROT:081897; EMBL:AL031394
A;Experimental source: cultivar Columbia; BAC clone T16L1
C;Genetics:
A;Map position: 4
A;Introns: 54/1; 117/3; 150/3; 415/3
A;Note: T16L1.300
                                                                                                                                                                                                                                                                                           Score 31; DB 2;
Pred. No. 24;
1; Mismatches
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Local Similarity 66.7%;
les 6; Conservative :
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 GANASSSFY 319
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A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Kohthors: Labragetein, G.; Krody, S.; Kumano, M.; Kurita, K.; Lapdus, A.; Hullo, M.F. Ayauthors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucelly, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schoceer, R.; Scoffone, F.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schoceer, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serox akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Tamaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, A; Authors: Yoshkawa, H.F.; Zumstein, E.; Yoshkawa, K.; Yasta, K.; Yasta, K.; Yoshida, K.; Yastunors: Yoshkawa, H.F.; Zumstein, E.; Yoshkawa, H.; Danchin, A. A; Ataus, R.; Yoshkawa, H.; Janchin, A.; Astaus: Peliminary; nucleic acid sequence not shown; translation not shown A; Reperence: UNIPROT: O34933; PMID: 9384377
A; Rose-references: UNIPROT: O34933; GB: Z99108; GB: AL009126; NID: g2631055; PIDN: CAB12580. C; Superimental source: strain 168
C; Superfamily: ferrichrome ABC transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clacession: T45786

Ribelseny, W., Berger, C., Cooke, R., Grellet, F.; Laudie, M.; Mewes, H.W.; Lemcke, abumitted to the Protein Sequence Database, December 1999

A;Reference number: 223013

A;Reference number: 223013

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1.895 - ADEL-

A;Cross-references: UNIPROT: 098CZ4; EMBL: AL133452

A;Experimental source: cultivar Columbia; BAC clone F26013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor-protein kinase-like protein - Arabidopsis thaliana
NyAlternate names: protein F26013.190
C;Species: Arabidopsis thaliana (mouse-ar cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.9%; Score 30; DB 2; Length 895; 66.7%; Pred. No. 72; 2; Indels tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.9%; Score 30; DB 1;
66.7%; Pred. No. 25;
tive 1; Mismatches 2
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Job time : 9.73529 secs
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A,Note: F26013.190
C,Superfamily: protein kinase homology
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Best Local Similarity 66.7.
---- 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                       probable membrane protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: 184428
C;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Recession: H8428
A;Reterence number: A84420; MUID:20083487; PMID:10617197
A;Rocession: H8428
A;Residues: 1-250 <STO-
A;Cross-references: UNIPROT:Q9ZUAS; GB:AE002093; NID:q4220472; PIDN:AAD12695.1; GSPDB:GN
A;Gene: Arzgol770
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description C18B10.10 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Orange 10-May-2001
C;Accession: C89103
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID: 99069613; PMID: 9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Accession: C89103
A;Accession: C89103
A;Accession: C89103
A;Residues: 1-291 cSTO>
A;Cross-references: GB:chr_V; PIDN:AAC25811.1; PID:g1699099; GSPDB:GN00023; CESP:C18B10.
C;Genetics:
A;Gene: C18B10.10
A;Map position: 5
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GOSB12

ferrichrome ABC transporter (permease) homolog yfmD - Bacillus subtilis

C;Species: Bacillus subtilis

C;Species: Do-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: C69812

R;Kunst, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C; Bron, S.; Brouiller, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; ChA.

A.; Brlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, B.

Nature 390, 249-256, 1997
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Pred. No. 22;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.9%; Score 30; DB 2; Length 250; 75.0%; Pred. No. 19; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.9%;
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 76.9
Best Local Similarity 75.0
Matches 6; Conservative
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                                 116 GADAKSSIF 124
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58 GANASSSI 65
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Gaps

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Length 333; 2; Indels ö

Gaps

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06ciu3 Kluyveromyc
0922t9 mus musculu
090658 gallus gall
P11438 mus musculu
080434 mus musculu
080434 mus musculu
080413 mus musculu
080413 rattus norv
03156 staphylococ
07a2n4 staphylococ
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07a2n4 staphylococ
07a2n4 staphylococ
02a92751 staphyloc
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xenopus lae
hordeum vul
cryza sativ
neurospora
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caenorhabdi
caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q89evl bradyrhizob
                                                                               October 26, 2004, 15:44:50 ; Search time 40.6324 Seconds (without alignments) 127.445 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
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08wga0
08s2e4
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                               1825181 seqs, 575374646 residues
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09CTU3
09CTU3
09CTU3
09CTU3
08VH34
LMP1 RAT
09DC13
06DC13
06DC13
06DC13
07AZN4
07AZN4
07AZN4
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CAE92757
CAE92757
Q8W459
UCR2 BOVIN
Q9FNJ5
Q81552
081552
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Maximum Match 100%
Listing first 45 summaries
                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAE92748
CAE92751
                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
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Q7YTU1
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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39
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Match Length DB
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Perfect score:
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                                                                                                                                                                       Sequence:
                                                                                    Run on:
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Q9HX10 Q9hX10 pseudomonas Q8PDC5 Q8pdc5 xanthomonas Q8PQ96 xanthomonas Q9ZUAS Q9ZUAS Q9ZUAS anabidopsis Q7ZBM2 Q728M2 emericella AAQ07985 AQ07985 emericella Q34BM3 Q94833 bacillus su Q5XEN7 Q9xen7 triticum ae Q6K489 CVFA89 satio BAD19896 Q9xen7 triticum ae Q6K489 Dad19896 cvyza sat Q8RGQ9 Q8rgq9 texbacter Q9HCF9 homo sapien Q7NIY1 Q8tbbc homo sapien Q8TBB6 homo sapien	153 AA. 153 AA. motation update) notation update) notation update) cobacteria; Rhizobiales; i., Iriguchi M., Kawashima K., Tsurucka H., Wada T., Yamada M., igen-fixing symbiotic bacterium D464AA94A490 CRC64; No. 8.5;	<pre>dismatches 1; Indels 0; Gaps 0;</pre>	PRT; 130 AA. eated) st sequence update) st annotation update) Saccharomycotina; Saccharomycetes; etaceae; Kluyveromyces.
Q9HX10 Q8PDC5 Q8PQ96 Q9ZUA5 Q7ZBM2 Q3ZBM3 Q9XEN7 Q6K489 Q6K489 Q6K489 Q6K489 Q6K489 Q6K489	PRT; 4, Createe 4, Last se 4, Last se 4, Last an 12597275; ato S., Mi 1088awa N Shimpo S., M 11 MW; 23C7 MW; 23C7 *; Score	.; H	PRI Creat Last Last Last Sac N; Sac
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2113 2226 2226 318 318 3334 401 401 708 708	IMINARY; MBLrel. 24 MBLRel.	rvativ F 9 F 81	MINARY; HBLrel. HBLrel. 19369; Ascomyo
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	PRELIM PRELIM PRELIM PRO13 (TrEMB 2003 (TrEMB 2003 (TrEMB Protein. ProcusNames= 20bium jap 1, Proteoba 1, Proteoba 1, Proteoba 1, Proteoba 1, Proteoba 222484998; 1053484998; 105378;	; Conserv GANAXSSLF : GANAQASLF	PRELIMI 004 (Trembi 004 (Trembi 004 (Trembi ty.
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STRAIN-CZECH II;
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KR Strausberg R.L.; Peingold E.A.; Grouse L.H., Derge J.G.;

KR Strausberg R.L.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;

RA Altschul S.F.; Zeeberg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

RA Altschul S.F.; Jordan H., Moore T., Max S.I.; Wang J., Haish F.;

RA Altschul S.F.; Jordan H., Moore T., Max S.I.; Wang J., Haish F.;

RA Altschul S.F.; Jordan H., Moore T., Max S.I.; Wang J., Haish F.;

RA Altschul S.F.; Jordan H., Moore T., Max S.I.; Wang J., Haish F.;

RA Brownstein M.J.; Usdin T.B.; Toshiyuki S., Carninci P., Prange C.,

RA Bosak S.A., McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;

R. Sichards S., Worley K.C.; Hale S., Garcia A.M.; Gay L.J.; Hulyk S.M.;

R. Nilalon D.K.; Muzny D.M.; Scdergren B.J.; Lu X.; Gibbs R.A.;

R. Hahey J., Helton E., Ketteman M.; Madan A.; Rodrigues S., Sanchez A.,

R. Hahey J., Helton E., Ketteman M.; Madan A.; Rodrigues S., Sanchez A.,

R. Ramanneki M.I.; Skalska U.; Schwutz J.; Myers R.M.; Butterfield Y.S.;

R. Jones S.J.; Marra M.A.;

R. Generation and initial analysis of more than 15,000 full-length human mean means and mouse onna
                                                                                                                                                                                                                                                                                                                                                                         ö
Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Blaykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boisrame A., Boyer E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
A. Swennene D., Tekaia F., Richard G.F., Streaub M.L., Suleau A.,
Bouchier C., Gaudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Wincker P., Souciet J.L.;
Mincker P., Souciet J.L.;
Mature 430:35-44(2004).
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                           Score 33; DB 2; Length 130;
Pred. No. 12;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                           Genoscope; Submitted (ULL-2004) to the EMBL/GenBank/DDBJ databases. EMBL; CR382126; CAG98854.1; -. SEQUENCE 130 AA; 14440 MW; A867F009FF5907BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse CDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel, 19, 01-DEC-2001 (TrEMBLrel, 19, 01-MAR-2004 (TrEMBLrel, 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lampl protein (Fragment).
Name=Lampl;
                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                  16 GANGISSLF 24
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                       1 GANAXSSLF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=NRRL Y-1140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its modified on profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Homeodomain protein ARR (Avian knotted-related protein).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
IISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ryan A.K., Tejada M.L., May D.L., Dubaova M., Deeley R.G.; "Isolation and characterization of the chicken homeodomain protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 23:3252-3259 (1995).

-i. FUNCTION: Binds to the F' element of the APOVLDLII gene and represses its transcription.

-i. SUBCELLULAR LOCATION: Nuclear.

-i. SIMILARITY: Belongs to the TALE/TGIF homeobox family.

-i. SIMILARITY: Contains 1 homeobox domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 2; Length 189;
Pred. No. 19;
0; Mismatches 2; Indels
                                                   R.; (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                          71F16D69BA4066FA CRC64;
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PROSITE; PSS0071; HOWEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein; Repressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269 AA.
                                                                  Submitted (APR-2001) to the EMBL/GenBank/DD
EMBL, BC006785, AH06785.1; -
MGD; MG1:96745; Lampl.
GO; GO:0005764; C:lysosome; IDA.
GO; GO:0005771; C:multivesicular body; IDA.
GO; GO:0042383; C:sarcolemma; IDA.
InterPro; IPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RANSFAC; T05163; -.
InterPro; IPR001356; Homeobox.
InterPro; IPR009057; Homeodomain_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95396587; PubMed=7667102;
                                                                                                                                                                                                                                                            PEGENT PRO1299; Lamp; 1.
PRINTS; PR00336; LYSASSOCTDMP.
PROSITE; PS00310; LAMP 1; 1.
PROSITE; PS00311; LAMP 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fram; PF00046; Homeobox; 1.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                             189 AA; 20456 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U25353; AAA83567.1; -.
PIR; S58439; S58439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 GMNASSSLF 71
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TRANSFAC; T05163; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GANAXSSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9031;
                                                Strausberg R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHICK
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKR CHI
Q90655;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
AKR_CHICK
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REQUINCE FROM N.A.

SEQUINCE FROM N.A.

REQUINCE FROM N.A.

STRAIN=C57BL/6; TISSUE=Brain;

X Trausner R.D., Feingold B.A., Grouse L.H., Derge J.G.,

RA Alteshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A plechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Alteshul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.

RA Soak S.A., McZwan P.J., McKernan K.J., Makek J.A., Gunaratne P.H.,

RA Kichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Niting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Schierleid Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA "Generation and initial analysis of more than 15,000 full-length human
                                                                                 .
                                                                                                                                                                                                     P11438; 062020;
01-0CT-1989 (Rel. 12, Created)
01-ACD-1990 (Rel. 15, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Lysosome-associated membrane glycoprotein 1 precursor (LAMP-1) (LGP-A)
(LGP-120) (CD107A) (P2B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 25-406 FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=88243722; Pubmed=3379044;
Chen J.W., Cha Y., Yuksel K.U., Gracy R.W., August J.T.,
"Isolation and sequencing of a cDNA clone encoding lysosomal membrane glycoprotein mouse LAMP-1. Sequence similarity to proteins bearing
                                                                               Gaps
                                                                                                                                                                                                                                                                               Name-Lamp): Synonyms-Lamp-1;
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                               "Characterization and cloning of lgp110, a lysosomal membrane glycoprotein from mouse and rat cells."; J. Biol. Chem. 265:12036-12043(1990).
                                                                                                                                                                                                                                                                                                                                                  [1] — SEQUENCE FROM N.A. MEDLINE=90307738; PubMed=2142158; Granger B.L., Green S.A., Gabel C.A., Howe C.L., Mellman I.,
                                                  Score 33; DB 1; Length 269;
Pred. No. 27;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Heffernan M., Yousefi S., Dennis J.W.;
Submitted (FEB-1990) to the EMBL/GenBank/DDBJ databases.
                Homeobox; TALE-type.
: 1074355DCC0C2253 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                               406 AA.
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J. Biol. Chem. 263:8754-8758(1988).
             35 97 H
269 AA; 29442 MW;
                                                 84.6%;
Transcription regulation.
DNA_BIND 35 97
SEQUENCE 269 AA; 29442
                                              Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
             Arterburn L.M., Earles B.J., August J.T.;
"The disulfide structure of mouse lysosome-associated membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lysosome-associated membrane glycoprotein
                                                 J. Biol. Chem. 265:7419-7423(1990).
-!- FUNCTION: Presents carbohydrate ligands to selectins. Also implicated in tumor cell metastasis.
-!- SUBCELLULAR LOCATION: Type I membrane protein. Lysosomal. This protein shuttles between lysosomes, endosomes, and the plasma
                                                                                                                                      -1- PTM: O- and N-glycosylated; some of the N-glycans attached to LAMP-1 are polylactosaminoglycans (By similarity).
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-> I (in Ref. 2 and 4).
ClbD373548BB9655 CRC64;
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Second lumenal domain.
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EMBL; M25244; AAA39428.1; ---
EMBL; BC049097; AAH49097.1; ---
EMBL; BC049097; AAH49097.1; ---
PIR; A28067; AAB39411.1; ---
PIR; A28067; AAB39411.1; ---
PIR; A60534; A60534.
MQD; MGI:96746; C.1. yoosome; IDA.
InterPro; IPR002000; Lamp.
Ffam; PR01299; Lamp; 1.
PRINTS; PR00336; LYSASSCTDMP.
PROSITE; PS00310; LAMP_1; 2.
MEDLINE=90237040; PubMed=2332434;
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MEDILINE=89017240; PubMed=3174652;
MEDILINE=89017240; FubMed=3174652;
Medilman I.;
Medilman I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                       Gaps
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01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Lysosome-associated membrane glycoprotein 1 precursor (LAMP-1) (120, kDa lysosomal membrane glycoprotein) (LGP-120) (CD107A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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  Length 406;
                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ono K., Han J.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AYO69998 AAL58070.1; -.
MGD; MGI:96745; Lampl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00336; LYSASSOCTDMP.
PROSITE; PS00310; LAMP 1; 2.
PROSITE; PS00311; LAMP 2; 1.
SEQUENCE 406 AA, 43879 MW; CIBD373548ADFA85 CRC64;
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GO; GO:0005771; C:multivesicular body; IDA.
GO; GO:0042383; C:sarcolemma; IDA.
InterPro; IPR002000; Lamp.
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                                    43;
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MEDLINE=89153580; PubMed=2920835;
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        84.6%;
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7; Conservative
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           Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lysosome-associated membrane glycoprotein
                                                                                                                                                                      -i- FUNCTION: Presents carbohydrate ligands to selectins. Also implicated in tumor cell metastasis.
-i- SUBCELLULAR LOCATION: Type I membrane protein. Lysosomal. This protein shuttles between lysosomes, endosomes, and the plasma
                                                                                                                                                                                                                                                     membrane.
-!- PTM: O and N-glycosylated; some of the N-glycans attached to LAMP-1 are polylactosaminoglycans (By similarity).
-!- SIMILARITY: Belongs to the LAMP family.
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Himeno M., Noguchi Y., Sasaki H., Tanaka Y., Furuno K., Kono Sakaki Y., Kato K.,
"Isolation and sequencing of a cDNA clone encoding 107 kDa sialoglycoprotein in rat liver lysosomal membranes.";
                                                                                                         SEQUENCE OF 283-357 FROM N.A. STRAIN=Wistar Kyoto, TISSUE=Aortic smooth muscle, STRAIN=Wistar Kyoto, TISSUE=Aortic smooth muscle, Adams L.A., Werny I., Schwartz S.M.; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D -> VT (in Ref. 3).
25947490749A7C88 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M14765; CAA38873.1; --
EMBL; X14765; CAA38873.1; --
EMBL; U17466; AB19108.1; --
PIR, A30200; A30200.
RGD; 2989; Lampl.
InterPro; IFR002000; Lamp.
Pfan; PF01299; Lamp; 1.
PRINTS; PR00316; LYSASSOCTDMP.
PROSITE; PS00310; LAMP. 1; 2.
PROSITE; PS00311; LAMP. 2; 1.
Glycoprotein; Lysosome; Signal; Transmembrane.
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FEBS Lett. 244:351-356(1989).
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329
356
407 AA;
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43969 MW;

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O1-UNV-2001 (TrEMBLrel. 17, Last sequence update)
01-UDN-2001 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
clone:1200007101 product:lysosomal membrane glycoprotein 1, full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-GSTBL/GJ; TISSUE=Lung;
STRAIN-GSTBL/GJ; TISSUE=Lung;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J; TISSUB=Lung;
MEDLINB=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1830 (2000).
                                        Gaps
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MEDLINE-20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoro R., Matsunnoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fuliwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watsuniki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                    Mus muscūlus (Mouse).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CS7BL/67, TISSUE=Lung;
MEDLINE=21085660, PubMed=11217851;
RIKEN FANTOM Consortium;
"Functional annotation of a full-length mouse cDNA collection.";
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             Score 33; DB 1; Length 407;
Pred. No. 43;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                            STRAIN=CS7BL/66; TISSUE=1ung;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
                                                                                                                                                      407 AA.
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             84.68;
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Lung;
PRELIMINARY;
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Nature 409:685-690(2001)
                                                                                     281 GMNATSSLF 289
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                                                              GANAXSSLF
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Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H., Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanadaki T., Hara A., Hayatsu N., Hiramock T., Hori F., Indean T., Hori F., Indean T., Hori F., Indean T., Asai J., Echii Y., Itch M., Izawa M., Kasukawa T., Kato H., Rawi J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Amai J., Kojima Y., Youno H., Kouda M., Koya S., Kurihara C., Sakai J., Nishi K., Nomara K., Numazaki R., Ohno M., Rasaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shibata Y., Sauni H., Tagawa A., Takahashi F., Tanaka T., Rasaki D., Shibata K., Shibata Y., Yoshida K., Shiraki T., Ragaba Y., Suzuki H., Tagawa A., Takahashi F., Tanaka T., Rasumateu W., Hayashizaki Y., Yasunishi A., Yoshida K., Yoshino M., Marameteu W., Hayashizaki Y., Sunishi K., Togawa A., Takahashi F., Tanaka T., Rami, McOdéo J., Baraza 1. J., Shibata K., Shibata K., Yoshino M., Rami, McOdéo J., Baraza 1. J., Shibata K., Shibata K., Yoshino M., Rami, Poloso J., Shibata K., Shibata K., Yoshino M., Roje Goloof 1. Shibata K., Shibata K., Yoshino M., Roje Goloof 1. Shibata K., Shibata K., Shibata K., Yoshino M., Roje Goloof 1. Shibata K., Shibata K., Yoshino M., Roje Goloof 1. Shibata K., Shibata K., Shibata K., Yoshino M., Roje Goloof 1. Shibata K., Shibata K., Shibata K., Yoshino M., Roje J., Shibata K., Shibata K., Shibata K., Yoshino M., Roje J., Shibata K., Shibata K., Shibata K., Yoshino M., Roje J., Shibata K., Yoshino M., Roje J., Shibata K., Shibata 
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Bell K.S., Sebaihia M., Pritchard L., Holden M., Hyman L.J.,
Bell K.S., Sebaihia M., Pritchard L., Holden M., Hyman L.J.,
Bell K.S., Sebaihia M.R., Bentley S.D., Churcher C., Mungall K.,
Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
Cormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
Salmond G.P.C., Birch P.R.J., Barrell B.G., Parkhill J., Torh I.K.,
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.

ENBL; EX950851; CAG76073.1; --
SEQUENCE 410 AA; 44608 MW; BZAD793237DE74F7 CRC64;
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Pectobacterium.
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Pred. No. 43;
0; Mismatches 2; Indels
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01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Maltose-binding periplasmic protein.
Name=malE; ORFNames=ECA3175;
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Pred. No. 44;
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01-JAN-1998 (
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STRAIN-gt31a-cp5;
Goorke C., Dasbadh S., Kuemmel M., Wolz C.;
Goorke C., Dasbadh S., Kuemmel M., Wolz C.;
and capin Staphylococcus aureus.";
submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
BMBL, AJ617715; CAE92745.1;
SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDILINE=21311952; PubMed=11418146; MEDILINE=21311952; PubMed=11418146; MEDILINE=21311952; PubMed=11418146; MEDILINE=21311952; PubMed=114.18146; Medicine T., Voriyama I., Baba T., Yuzawa H., Kobayashi I., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goro S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba 'Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; Staphylococcus aureus.";
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                                                                                                                                                                                                                                                                                                                                                                                         Name-agrD; OrderedLocusNames-SA1842.1; ORFNames=SAS066; Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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01-APR-2004 (TrEMBLrel. 27, Last sequence update)
01-APR-2004 (TrEMBLrel. 27, Last annotation update)
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
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EMBL, AP003135, BAB43124.1; -.
InterPro; IPR009229; AgrD.
Pfam; PF05931; AgrD. 1.
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                       STRAIN=SA502A;
MEDLINE=97342847; PubMed=9197262;
MIDLINE=97342847; Novick R.P.;
"Bacterial interference caused by autoinducing peptide variants.";
Science 276:2027-2030(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Gt31a-cp5, Gt31b-cp5, Gt36a-cp8, Gt36b-cp8, and Gt111-cp8; Goerke C., Dasbach S., Kuemmel M., Wolz C.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 7.1;
0; Mismatches 2; Indels
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Staphylococcus aureus (strain Mu50 / ATCC 700699).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158878;
                                                                                                                           Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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EMBL; AJ617715; CAE92745.1;
EMBL; AJ617715; CAE92748.1;
EMBL; AJ617717; CAE92751.1;
EMBL; AJ617718; CAE92754.1;
EMBL; AJ617719; CAE92757.1;
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InterPro; IPR009229; AgrD.
Pfam; PF05931; AgrD; 1.
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   01-JAN-1998 (TremBLrel. 05, 01-OCT-2004 (TremBLrel. 28,
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                                                                                                                                                                        NCBI_TaxID=1280;
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STRAIN=gtllb-cp5;
STRAIN=gtllb-cp5;
STRAIN=gtllb-cp5;
"Evolutionary Models for the Development of the Polymorphic Loci agr and cap in Staphylococcus aureus.";
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
BENBL; AJ617716; CAE9274811, -.
SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;
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Goerke C., Dasbach S., Kuemmel M., Wolz C.;
"Evolutionary Models for the Development of the Polymorphic Loci agr and cap in Staphylococcus aureus.";
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ617717; CAE92751.1;
SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;
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82.1%; Score 32; DB 2; Length 47;
Best Local Similarity 77.8%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 2; Indels
                                                                                                                                 01-AFR-2004 (TrEMBLrel. 27, Created)
01-APR-2004 (TrEMBLrel. 27, Last sequence update)
01-APR-2004 (TrEMBLrel. 27, Last annotation update)
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01-APR-2004 (TrEMBLrel. 27, Last sequence update)
01-APR-2004 (TrEMBLrel. 27, Last annotation update)
AgrD protein.
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Bacteria, Firmicutes; Bacillales, Staphylococcus.
NCBI_TaxID=1280;
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RESULT 1
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Length DB ID	4.6 9 3 AAY67853 A	4.6 9 5 AAM50901 Aam50901	4.6 9 5 ABP53542	3.8 163 5 ABU05504 Abu05504	3.8 167	3.8 167 6 ABF57498 Abp57498	1.1 9 3 AAY67860 Aay67860	1.1 9 3 AAY67859 Aay67859	1.1 9 5 ABB07160 Abb07160	1.1 9 5 AAM50907 Aam50907 Protec	1.1 9 5 AAM51004 AgrD2	1.1 9 5 AAM51003 AgrD2	1.1 9 5 AAM51002 AgrD2	1.1 28 4 ABG15689 Abg15689	1.1 332 7 ABO83045	1.1 347 7 ADC96234 Adc96234	1.1 367 6 ABU29795 Abu29795	1.1 543 2 AAY33146 Aay33146	1.1 .546 8 ADP87483 Adp87483	1.1 564 8 ADP87485 Adp87485 Rabbit	1.1 565 2 AAY33145	1.1 565 8 ADG98216 Abbit	1.1 566 3 AAB08202	1.1 2243
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AAY67851	ABB07161	AAM51005	AAM50908	AAM50899	ABP53540	AAB19724	ADD18295	AAB19725	ADD18297	ABG09243	AAW38323	ABB07159	AAM51001	ABB84631	ADF09190	ADJ98875	AAR37301	AAB44017
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ALIGNMENTS

first entry) ide #3 used for bacterial int aureus infection; cyclic pep or; treatment. Location/Qualifiers /note= "N-terminal residue residue to form a cyclic pe /set of form a cyclic pe per page of form a cyclic pe /label= Unknown /label= Unknown cockBFELLER. BW YORK STATE. ille P, Novick RP, Ji G, E cockBFELLER. itle P, Novick RP, Ji G, E cockBFELLER. i		
25-APR-2000 (first entry) S. aureus peptide #3 used for bacterial interference. Staphylococcus aureus infection; cyclic peptide; AgrD; agr virulence factor; treatment. Staphylococcus aureus. Key Modified-site Location/Qualifiers		
S. aureus peptide #3 used for bacterial interference. Staphylococcus aureus infection; cyclic peptide; AgrD; agr virulence factor; treatment. Staphylococcus aureus. Key Location/Qualifiers Modified-site Location/Qualifiers Modified-site Location/Qualifiers Fesidue to form a cyclic peptide" Fesidue to form a cyclic peptide" Jabel= Unknown W09967286-A2. 29-DEC-1999. 24-JUN-1999; 99WO-US014562. 24-JUN-1999; 99WO-US01438. (UYRQ) UNIV ROCKEFELLER (UTRQ) UNIV ROCKEFELL	25-APR-2000	
Staphylococcus aureus infection; cyclic peptide; AgrD; agr virulence factor; treatment. Staphylococcus aureus. Key Modified-site 1 / note= "N-terminal residue forms bond with residue to form a cyclic peptide" / label= Unknown W09967286-A2. 29-DEC-1999. 24-JUN-1998; 98US-00103438. 24-JUN-1998; 98US-00103438. (UYRQ) UNIV ROCKEFELLER. (UTRQ) UNIV	S. aureus peptide #3 used for bacterial	
Staphylococcus aureus. Key Modified-site 1	Staphylococcus aureus infection, cyclic peptide, AgrD, agr virulence factor, treatment.	response;
Modified-site 1	Staphylococcus	
Misc-difference 5 / Jabel= Unknown W09967286-A2. 29-DEC-1999. 24-JUN-1998; 98US-00103438. (UYRQ) UNIV ROCKEFELLER. (UYRQ) UNIV ROCKEFELLER. (UYRQ) UNIV ROCKEFELLER. Muir TW, Mayville P, Novick RP, Ji G, Beavis R; WPI; 2000-147202/13. New cyclic peptides for treating infections with Staphyloco Claim 9; Page 26; 37pp; English. This sequence represents a cyclic peptide derived from the aureus AgrD peptide. The invention relates to AgrD derived composition containing a peptide and a carrier, and a metho production of the cyclic peptides. The peptide inhibits the which is normally associated with the release of virulence Staphylococcus aureus. An AgrD peptide is produced by S. au	Key Locatio Modified-site 1 /note=	C-terminal
W09967286-A2. 29-DEC-1999. 24-JUN-1999; 99WO-US014562. 24-JUN-1999; 98US-00103438. (UVRQ) UNIV ROCKEFELLER. (UVRQ) UNIV NEW YORK STATE. Muir TW, Mayville P, Novick RP, Ji G, Beavis R; WPI; 2000-147202/13. New cyclic peptides for treating infections with Staphylococlaim 9; Page 26; 37pp; English. This sequence represents a cyclic peptide derived from the aureus AgrD peptide. The invention relates to AgrD derived composition of the cyclic peptide and a carrier, and a metho production of the cyclic peptide in the release of virulence staphylococcus aureus. An AgrD peptide is produced by S. au	Misc-difference 5 /label=	
29-DEC-1999. 24-JUN-1999; 99WO-US014562. 24-JUN-1998; 98US-00103438. (UVRQ) UNIV ROCKEFELLER. (UVNY) UNIV NEW YORK STATE. Muir TW, Mayville P, Novick RP, Ji G, Beavis R; WPI; 2000-147202/13. New cyclic peptides for treating infections with Staphyloco Claim 9; Page 26; 37pp; English. This sequence represents a cyclic peptide derived from the aureus AgrD peptide. The invention relates to AgrD derived composition of the cyclic peptide and a carrier, and a metho production of the cyclic peptides. The peptide inhibits the which is normally associated with the release of virulence Staphylococcus aureus. An AgrD peptide is produced by S. au		
24-JUN-1999; 99WO-US014562. 24-JUN-1998; 98US-00103438. (UVRQ) UNIV ROCKEFELLER. (UVRY) UNIV NEW YORK STATE. Muir TW, Mayville P, Novick RP, Ji G, Beavis R; WPI; 2000-147202/13. New cyclic peptides for treating infections with Staphyloco Claim 9; Page 26; 37pp; English. This sequence represents a cyclic peptide derived from the aureus AgrD peptide. The invention relates to AgrD derived composition containing a peptide and a carrier, and a metho production of the cyclic peptides. The peptide is methop which is normally associated with the release of virulence Staphylococcus aureus. An AgrD peptide is produced by S. au		
24-JUN-1998, 98US-00103438. (UVRQ) UNIV ROCKEFELLER. (UVRY) UNIV NEW YORK STATE. Muir TW, Mayville P, Novick RP, Ji G, Beavis R; WPI; 2000-147202/13. New cyclic peptides for treating infections with Staphyloco Claim 9; Page 26; 37pp; English. This sequence represents a cyclic peptide derived from the aureus AgrD peptide. The invention relates to AgrD derived composition containing a peptide and a carrier, and a metho production of the cyclic peptides. The peptide inhibits the which is normally associated with the release of virulence Staphylococcus aureus. An AgrD peptide is produced by S. au	24-JUN-1999;	
(UVRQ) UNIV ROCKEFELLER. (UVNY) UNIV NEW YORK STATE. Muir TW, Mayville P, Novick RP, Ji G, Beavis R; WPI; 2000-147202/13. New cyclic peptides for treating infections with Staphyloco Claim 9; Page 26; 37pp; English. This sequence represents a cyclic peptide derived from the aureus AgrD peptide. The invention relates to AgrD derived composition containing a peptide and a carrier, and a metho production of the cyclic peptides. The peptide inhibits the which is normally associated with the release of virulence Staphylococcus aureus. An AgrD peptide is produced by S. au	24-JUN-1998;	
Muir TW, Mayville P, Novick RP, Ji G, Beavis R; WPI; 2000-147202/13. New cyclic peptides for treating infections with Staphyloco Claim 9; Page 26; 37pp; English. This sequence represents a cyclic peptide derived from the aureus AgrD peptide. The invention relates to AgrD derived composition containing a peptide and a carrier, and a metho production of the cyclic peptides. The peptide inhibits the which is normally associated with the release of virulence Staphylococcus aureus. An AgrD peptide is produced by S. au	(UYRQ) UNIV (UYNY) UNIV	
WPI; 2000-147202/13. New cyclic peptides for treating infections with Staphyloco Claim 9; Page 26; 37pp; English. This sequence represents a cyclic peptide derived from the aureus AgrD peptide. The invention relates to AgrD derived composition containing a peptide and a carrier, and a metho production of the cyclic peptides. The peptide in hibbits the which is normally associated with the release of virulence Staphylococcus aureus. An AgrD peptide is produced by S. au	Muir TW, Mayville P, Novick RP, Ji G, Beavis	
New cyclic peptides for treating infections with Staphyloco Claim 9; Page 26; 37pp; English. This sequence represents a cyclic peptide derived from the aureus AgrD peptide. The invention relates to AgrD derived composition containing a peptide and a carrier, and a metho production of the cyclic peptides. The peptide inhibits the which is normally associated with the release of virulence Staphylococcus aureus. An AgrD peptide is produced by S. au	WPI;	
Claim 9; Page 26; 37pp; English. This sequence represents a cyclic peptide derived from the aureus AgrD peptide. The invention relates to AgrD derived composition containing a peptide and a carrier, and a metho production of the cyclic peptides. The peptide inhibits the which is normally associated with the release of virulence Staphylococcus aureus. An AgrD peptide is produced by S. au	New cyclic peptides for treating infections with	
This sequence represents a cyclic peptide derived from the aureus AgrD peptide. The invention relates to AgrD derived composition containing a peptide and a carrier, and a metho production of the cyclic peptides. The peptide inhibits the which is normally associated with the release of virulence Staphylococcus aureus. An AgrD peptide is produced by S. au	Claim 9; Page 26; 37pp;	
	This sequence represents a cyclic peptide derived from the aureus AgrD peptide. The invention relates to AgrD derived composition containing a peptide and a carrier, and a metho production of the cyclic peptides. The peptide inhibits the which is normally associated with the release of virulence Staphylococcus aureus. An AgrD peptide is produced by S. au	Staphylococcus peptides, a d for the agr response, factors of reus that

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Query Match
Best Local Similarity
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                                                                                                                                                            Sequence 9 AA;
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24-JUN-1999;
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                                                                                                                      infection
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(JIGG/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of a novel synthetic cyclic peptide of the invention that is capable of inhibiting the agr response of staphylococcus aureus. It is an AgrD-autoinduring peptide, where AgrD is secreted agr-encoded peptide and where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. Preferred peptides may have residue and COOH other than a thioester bond, where X is an amino acid, an amino acid analogue, a peptidominetic or non-amide isostere, Z is a synthetic or a biosynthetic amino acid, n is 0-10 and y is 1-10. The cyclic bond is especially a lactam or lactone bond. The thiololaccone structure within native AgrD peptides is required for activation of the structure can destroy agr response activating activity while preserving and enhancing inhibitory activity. A claimed method of preparing a cyclic
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with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus {\sf conposition} in the peptides of the strain of the peptides of the strain of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "note linked to residue 9 to form cyclic peptide"
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                                                                                                                                         Gaps
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                                                                                                  Length 9;
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                                                                                                  94.6%; Score 35; DB 3; Le 100.0%; Pred. No. 1.7e+06;
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                                                                                                                                                                                                                                                                                                                  AAM50901 standard; peptide; 9
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(UYNY ) UNIV NEW YORK STATE.
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                                                                                                                                           Conservative
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Matches 9; Conserv
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                                                          Sequence 9
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peptide involves; assembling a linear peptide chain on to a solid phas resin support; deprotecting the resulting protected assembled peptide; treating the deprotected peptide with neutral buffer for a time sufficient to form the cyclic peptide and cleave the peptide from the support; and recovering the cyclic peptide. The peptide is useful for bacterial interference, especially for the treatment of S. aureus
                                                                                                                                                                                                                                                                                                     Gaps
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infections.
                                                                                                                                                                                                                                               94.6%; Score 35; DB 5; Length 9; 100.0%; Pred. No. 1.7e+06; ive 0; Mismatches 0; Indels
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Pred. No. 1.7e+06;
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100.0%;
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                                                                                                                                                                                                                                                                                                  9; Conservative
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MAYVILLE P.
NOVICK R P.
BEAVIS R.
JI G.
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Matches 9; Conserv
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Matches

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This invention relates to a novel method for identifying essential genes for survival or virulence of mycobacteria species. The method comprises aligning the genomic sequence of a first mycobacterium species on a genomic sequence of a second mycobacterium species and selecting a polymucleotide sequence that is highly conserved in both genomes with no counterparts in other bacterial genomic sequences and that corresponds to an essential gene for the survival or virulence of mycobacterium species. The method of the invention is useful for detecting M. tuberculosis or M. Impare infection. The method reduces the number of potential new targets and prevent mycobacterial diseases, particularly tuberculosis and mycobacterium tuberculosis and Mycobacterium tuberculosis and Mycobacterium teprae identified using the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying and selecting genes for survival or virulence of mycobacteria by a comparative genomic analysis of the sequences of Mycobacterium tuberculosis and M. leprae.
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                                                                                                         Mycobacterioses; survival; virulence; protective antigen; vaccine; mycobacterial disease; tuberculosis; leprosy.
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Pred. No. 44;
0; Mismatches 2; Indels
                                                                       M. tuberculosis and M. leprae marker protein #538.
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Mycobacterium leprae.
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Matches
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  Indels
                                                                                                                                                                                                                                                                                                 M. tuberculosis and M. leprae marker protein #155.
  ;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU05887 standard; protein; 167 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Page 331; 874pp; English.
                                                                                                                                                                                 ABU05504 standard; protein; 163 AA.
  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-FEB-2002; 2002WO-IB001973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-FEB-2001; 2001US-0270123P
                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis.
Mycobacterium leprae.
                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 77.8
Matches 7; Conservative
    9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVAAASSAF
                                          GVAAXSSLF
                                                               GVAAXSSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200274903-A2.
                                                                                                                                                                                                                                                                08-APR-2003
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                                                                                                                                                                                                                       ABU05504;
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Cole S;

RESULT S ABU05887 ID ABU0 XX

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Gaps

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(MICR-) MICROBIOLOGICAL RES AUTHORITY

Marsh P;

Bacon J,

James BW,

WPI; 2003-201403/19 N-PSDB; ABZ71124

21-JUN-2002; 2002WO-GB002845.

WO2003000721-A2.

03-JAN-2003

22-JUN-2001; 2001GB-00015365.

Claim 2; Page 230; 246pp; English.

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This sequence represents the Staphylococcus aureus AgrDII derived peptide. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the Staphylococcus aureus AgrDII derived peptide. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus
                                                                                   New cyclic peptides for treating infections with Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New cyclic peptides for treating infections with Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus infection; treatment; AgrD; agr response;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30; DB 3; Length 9;
Pred. No. 1.7e+06;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus AgrDII derived peptide seguence.
  Beavis R;
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Novick RP,
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                                                                                                                               Example; Page 22; 37pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                         81.1%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US014562,
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(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 77.40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
Mayville P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Muir TW, Mayville P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GVAAXSSLF 9
                                            WPI; 2000-147202/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-147202/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GVNASSSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    virulence factor
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9 AA;
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ŢW,
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Muir,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                   useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABPS7436 to ABPS7504 represent mycobacterial amino acid sequences (I) encoded by ABZ71062 to ABZ71130 (II), which are isolated from Mycobacterium tuberculosis. (I) are encoded by ganes (II) whose expression is induced or up-regulated during culture of a mycobacterium under conditions defined by a dissolved oxygen tension of at least 10% air saturation measured at 37 plus degrees Celsius, when compared with a dissolved oxygen tension of at least 40% air saturation measured at 37 plus degrees Celsius, under compared with a plus degrees Celsius. (I) and (II) have antibacterial, tuberculostatic and immunostimulant activities, and can be used in vaccines and gene therapy. (I) and (II) can be used for the manufacture of a medicament for treathing or preventing a mycobacterial infection. They can also be used for the manufacture of a diagnostic reagent for identifying a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                              New mycobacterial peptide, its fragment, variant or derivative, use:
vaccine for treating or preventing mycobacterial infections, and as
diagnostic reagents for identifying such infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus infection; AgrD; agr response; treatment;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.8%; Score 31; DB 6; Length 167; 77.8%; Pred. No. 44; 2; Indels ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus AgrDII derived peptide sequence.
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AAY67860 standard; peptide; 9 AA

GVAAASSAF 144

136

RESULT

1 GVAAXSSLF 9

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Query Match Best Local Similarity 77.8 Best Local 7; Conservative

mycobacterial infection

Sequence 167 AA;

(first entry)

25-APR-2000

AAY67860;

Staphylococcus aureus

WO9967286-A2

29-DEC-1999,

virulence factor.

98US-00103438 99WO-US014562

24-JUN-1999; 24-JUN-1998; ROCKEFELLER. NEW YORK STATE.

(UYRQ) UNIV

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Gaps

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Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic; antibacterial; infection; therapy; cyclic.
                                          AAM50907 standard; peptide; 9 AA.
                                                                                                                                                                                                                                     Key
Modified-site
                                                                      AAM50907;
                            AAM50907
                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to the use of autoinducer-2 (AI-2) agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis. Synergistic antiblotic compositions comprising inhibitors of the quorum-sensing pathway of a microorganism are also provided. Methods using such AI-2 analogues are useful for tracting pathogen-associated disease states. The compounds and antibiotic compositions can be used to inhibit bacterial cell growth and/or biofilm formation on a medical device, particularly for promoting growth of skin graft replacements used in the treatment of burns and ulcers. They may also be used to aid wound repair, and to inhibit bacterial cell growth and biofilm formation in or on products or devices used for personal hygiene. The present sequence represents a inhibitor of peptide-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of autoinducer-2 agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis, also antibiotic compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shokat K, Stein J, Surette MG;
                                                          Gaps
                                                                                                                                                                                                                                                                                                                           vulnerary; pheromone; agr system; accessory gene regulator; cyclic.
                                                                                                                                                                                                                                                                                                             Autoinducer-2; AI-2; antibiotic; antibacterial; dermatological;
                                                          ..
0
                                                                                                                                                                                                                                                                               Peptide-mediated quorum sensing inhibitor peptide cyclo-XII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30; DB 5; Length 9;
Pred. No. 1.7e+06;
); Mismatches 2; Indels
                          Score 30; DB 3; Length 9;
Pred. No. 1.7e+06;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schauder S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 33; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYPR-) UNIV PRINCETON.
(QUOR-) QUOREX PHARM INC.
(UYTE-) UNIV TECHNOLOGIES INT INC.
                                                                                                                                                                                         ABB07160 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.1%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAY-2001; 2001WO-US015221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0203000P
                            81.18;
77.88;
                                                                                                                                                                                                                                                   (first entry)
                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bassler BL, Dammel CS,
                                                                                      σ
                                                                                                                σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-075235/10.
                                                                                    1 GVAAXSSLF
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Best Local Similarity
Matches 7; Conserv
                                                                                                                1 GVNAASSLF
                                        Local Similarity
nes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quorum sensing
Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAY-2000;
07-DEC-2000;
                                                                                                                                                                                                                                                   13-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                 15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                     ABB07160;
                          Query Match
                                           Best Loc
Matches
                                                                                                                                                            RESULT 9
                                                                                                                                                                              ABB07160
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/note= "note linked to residue 5 to form cyclic peptide"

'note=

Misc-difference

US6337385-B1 08-JAN-2002.

/note= /note=

Ü J.

Beavis R,

Muir TW, Mayville P, Novick RP,

WPI; 2002-170774/22.

(UYRQ) UNIV ROCKEFELLER. (UYNY) UNIV NEW YORK STATE.

99US-00339511. 98US-0090402F.

24-JUN-1999; 24-JUN-1998;

"note linked to residue 9 to form cyclic peptide"

"Ser(tBn)" "Ser(Bzl)" "Ser(Bzl)"

Location/Qualifiers

Synthetic

/note= "Z-Gly"

'note=

Misc-difference

Modified-site Modified-site Modified-site

Protected peptide used in cyclic peptide production.

(first entry)

08-MAY-2002

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The present sequence is that of a protected peptide used in an example of the preparation of novel synthetic cyclic peptides of the invention (see AAMS0899-906). The peptide corresponds to the Staphylococcus aureus aground a Cys5 to Ser mutation (lactone). It was synthesised on a Wang-resin using an Fmoc N-alpha protection strategy. Following con a Mang-resin using an Fmoc N-alpha protection strategy. Following contain assembly, the peptide was cleaved from the support and the Ser-5 residue deprotected by treatment with a trifluoroacetic addianisole water mixture (90:5:5) for 4 hr. The partially protected peptide-alpha carboxylates were then dissolved in DMF and treated with complete after 2 hr. The remaining protecting groups were then removed by treatment with HF and the peptide purified by HPLC. The cyclic peptide is capable of inhibiting the agr response of Staphylococcus aureus. The thiololactone structure within native AgrD peptides is required for activation of this response. Replacement of the thiol ester component of the cyclic ring structure with a lactone (as in the present case) or a lactam can destroy activity. The cyclic peptides are useful for enhancing inhibitory activity. The cyclic peptides are useful for the contains interference, especially for the treatment of S. aureus
Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in a
                                                                                                                                                                                                                                                     Disclosure; Col 14; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infection
                                                                                                                                                subject.
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Sequence 9 AA;

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GVAAXSSLF

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GVNASSSLF

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of a novel synthetic AgrD2 lactone cyclic peptide in which residue 5 of the peptide is linked to residue 9 via a lactone bond. The peptide is derived from an AgrD2 peptide 0 via a station of the peptide is derived from an AgrD2 peptide of staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other carracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthesic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agrP3 promoter. This allowed activation or inhibition of the agr response to be monitored spectrophotometrically. The lactone AgrD2 peptide inhibited the agr response of group I S. aureus strains without culturating the agr response of group I S. aureus strains without provides claimed cyclic peptides (see AAMS0899-906 and AMMS0899) and methods for preparing them, especially peptides where the cyclic bond is a lactam or lactone bond. The cyclic peptides are useful for bacterial interference, especially for the treatment of S. aureus infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "note linked to residue 9 to form cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AgrD2, agr response; inhibitor; antibiotic; antibacterial; infection; therapy; lactone; cyclic.
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in a subject.
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Query Match 81.1%; Score 30; DB 5; Length 9; Best Local Similarity 77.8%; Pred. No. 1.7e+06; Matches 7; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ji G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novick RP, Beavis R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                          AAM51004 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Col 9; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0090402P.
                                                                                                                                                                                                                                                                                                                                                                                                                             AgrD2 lactone cyclic peptide
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(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                         (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus.
Synthetic.
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                                                                                            1 GVAAXSSLF 9
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                                                                                                                                       1 GVNASSSLF
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Misc-difference
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08-MAY-2002
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                                                                                                                                                                                                                                                                                                            AAM51004;
                                                                                                                                                                                                                RESULT 11
                                                                                                                                                                                                                                    AAMS1004
AAM
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The present sequence is that of a novel synthetic AgrD2 linear free acid peptide. The peptide is derived from the cyclic AgrD2 peptide of stapping between the peptide is derived from the cyclic AgrD2 peptide of stapping controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured is areas strains containing a beta-lactamase reporter gene fused to the agr3 promoter. This allowed activation or inhibition of the agr response to be monitored spectrophotometrically. Unlike an AgrD2 thiololactone cyclic peptide (see Awh51001), the present peptide was unable to either activate or inhibit the agr response, even when added to cultured cells at UM concentrations. The invention provides claimed cyclic peptides (see Awh51001) and methods for preparing them. The cyclic peptides are useful for bacterial interference, especially for the treatment of S. aureus infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in a
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0
                                                    2; Indels
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  Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
Score 30; DB 5; I
Pred. No. 1.7e+06;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beavis R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novick RP,
                                                                                                                                                                                                                                                                                          AAM51003 standard; peptide; 9 AA.
                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AgrD2 linear free acid peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Col 9; 18pp; English
     81.1%;
77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYRQ ) UNIV ROCKEFELLER.
(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                           Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muir TW, Mayville P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-170774/22.
                                                                                                         1 GVAAXSSLF
                                                                                                                                                           GVNASSSLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6337385-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                 08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                               AAM51003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   subject.
                                                                                                                                                                                                                                      RESULT 12
                                                                                                                                                                                                                                                                    AAM51003
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08-MAY-2002

therapy

AAM51002;

RESULT 13 AAM51002 24-JUN-1999; 24-JUN-1998;

US6337385-B1 08-JAN-2002.

us-10-032-950-3.rag

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCN) primers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed continuous is useful in gene therapy techniques to restore normal cutivity of (II) are to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and its binding partners are useful for treating disorders of sites expressing (II). (I) and its binding partners are useful for treating disorders of polypeptide and polynucleotide sequences have applications in diagnostic formsics, formsics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                     Human, chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.1%; Score 30; DB 4; Length 28; 77.8%; Pred. No. 11; 2; Indels iive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID NO 46048; 103pp; English.
                                                                                          Novel human diagnostic protein #15680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABO83045 standard; protein; 332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                        30-MAR-2001; 2001WO-US008631.
                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 77...
7; Conservative
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N-PSDB; AAS79876.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVAAGMSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 28 AA;
                                                                                                                                                                                                                                                         WO200175067-A2.
                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   biodiversity.
                                               18-FEB-2002
                                                                                                                                                                                                                                                                                                        11-OCT-2001.
ABG15689;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of a novel synthetic AgrD2 linear thioester peptide. The peptide is derived from the cyclic AgrD2 peptide of Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agr P3 promoter. This allowed activation or inhibition of the agr response to be monitored spectrophocometrically. Unlike an AgrD2 thiololatone correction of the peptide was unable to either activate or inhibit the agr response, even when added to cultured cells at UM concentrations. The invention provides claimed cyclic peptides (see AAM50999) and methods for preparing them. The cyclic peptides are useful for bacterial interference, especially for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                           AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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Pred. No. 1.7e+06;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beavis R,
                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muir IW, Mayville P, Novick RP,
                                                                      AAM51002 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Col 9; 18pp; English.
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                                                                                                                                                                                                              AgrD2 linear thioester peptide.
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Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-00339511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0090402P
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(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-170774/22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9 AA;
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Modified-site
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subject.

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Gaps

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RESULT 14
ABG15689
ID ABG15
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The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and the polynucleotides encoding them. The sequences are useful in diagnosis and the pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bhid a P aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of freedomonant species using biochip technology. Sequences ABO67826-
of Pseudomonas species using biochip technology. Sequences ABO67826-
sequence data for this patent did not form part of the invention. Note: The specification but was obtained in electronic format from USPFO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                            Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.1%; Score 30; DB 7; Length 332; 66.7%; Pred. No. 1.5e+02; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                            Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 31791; 455pp; English.
                                         Pseudomonas aeruginosa polypeptide #15220.
                                                                                                                                                                                                                                                                                                                                                                            Deloughery C,
                                                                                                                                                                                                                                                                                                                                  (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                     99US-00252991
                                                                                                                                                                                                                                                                         98US-0074788P.
                                                                                                                                                                                                                                                                                                                                                                          Rubenfield MJ, Nolling J,
  29-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                   Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-615309/58.
N-PSDB; ABD16616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 332 AA;
                                                                                                                                                         US6551795-B1
                                                                                                                                                                                                                                     18-FEB-1999;
                                                                                                                                                                                                                                                                         18-FEB-1998;
27-JUL-1998;
                                                                                                                                                                                                22-APR-2003.
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Search completed: October 26, 2004, 15:59:41 Job time: 43.75 secs

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Sequence 3. Appli
Sequence 155. App
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Sequence 155. App
Sequence 538. App
Sequence 538. App
Sequence 538. App
Sequence 153774.
Sequence 153774.
Sequence 151015,
Sequence 37015, A
Sequence 37015, A
Sequence 37015, A
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                                                                                                                                  October 26, 2004, 15:54:00 ; Search time 31.5 Seconds (without alignments) 92.502 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
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4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
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10: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
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10: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-156-761-9222
US-10-080-170-155
US-10-080-170-155
US-10-080-170-155
US-10-080-170-538
US-10-080-170-538
US-10-470-538
US-10-470-55-538
US-10-470-55-538
US-10-470-55-538
US-10-767-701-463-52
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Maximum Match 100%
Listing first 45 summaries
                                                                                        - protein search, using sw model
                                                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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37
1 GVAXXSLF 9
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Match Length
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                                                                                                                                         Run on:
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Sequence 2, Appli Sequence 11, Appli Sequence 151465, Sequence 37550, A Sequence 10, Appl Sequence 10, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 18140, Sequence 18140, Sequence 18140, Sequence 18140, Sequence 3, Appli Sequence 3, Appli Sequence 21463, Sequence 21463, Sequence 21463, Sequence 21463, Sequence 3838, Appli Sequence 5455, Sequence 5455, Sequence 5455, Sequence 5455, Sequence 53319, Appli Sequence 53319, Appli	BACTERIAL e: Synthetic this position.
US-10-267-756-2 US-10-032-950-1 US-10-437-950-1 US-10-437-950-146327. US-10-767-701-37550 US-09-966-546-10 US-09-966-546-10 US-09-966-546-12 US-10-437-963-183290 US-10-427-91-181290 US-10-427-91-181290 US-10-427-91-181290 US-10-427-91-181290 US-10-427-91-181290 US-10-427-91-4675 US-10-424-599-242903 US-10-424-599-242903 US-10-424-599-242903 US-10-424-599-24459303 US-10-424-599-24459303 US-10-425-114-59515 US-10-425-114-59519 US-10-425-114-59519 US-10-205-219-67	IGNMENTS COCCUS PEPTIDES FOR 032,950 Artificial Sequence any amino acid at t
000000000111111818000117	n US/10032950 0077453A1 Patricia 20077453A1ick, onald YONE TIRRFERENCE 1NTRRFERENCE 1NTRRFERENCE 2010-12-27 2010-12-27 98-06-24 98 x. 2.0 sequence escription of
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	-950-3 -950-3 -100 No. US20 INFORMATION: ANT: Mary To ANT: Mary To ANT: No. US2 ANT: Beavis, ANT: APPLICATION: APPLICATION: APPLICATION: APPLICATION: ANT: BEBREAUTION: ANT: ANT: ANT: ANT: ANT: ANT: ANT: ANT:
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Gaps

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Query Match
94.6%; Score 35; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels

1 GVAAXSSLF 9

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Sequence 155, Application US/10080170 Publication No. US20040121322A9 GENERAL INFORMATION:
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US-10-080-170-538
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TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
TITLE OF INVENTION: TERATHENT OF MYCOBACTERIOSES
FILE REPERENCE: 03495.0218
CURRENT APPLICATION NUMBER: US/10/080,170
FRICH SPLING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 652
SOFTWARE: PALCHIN VET. 2.1
SEQ ID NO 155
LENGTH: 163
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                                                                                                                                                                                     APPLICANT: ONURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIRAM, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATYORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
SQ ID NO 9222
                                                                                                                               Sequence 9222, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-080-170-155
; Sequence 155, Application US/10080170
; Publication No. US20030129601A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9222
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; ORGANISM: Mycobacterium leprae
US-10-080-170-155
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Best Local Similarity 77.8
Matches 7; Conservative
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Matches 7; Conservative
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  GVAAXSSLF 9
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US-10-156-761-9222
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US-10-080-170-155

RESULT

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Sequence 155, Application US/10468356
Publication No. US20040197896A1
GENERAL INFORMATION:
TENDICANT: COLE, STEWART
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENEOMICS AS A TOOL FOR
TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
TILE REFERENCE: 05394.0019
CURRENT APPLICATION NUMBER: US/10/468,356
CURRENT FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: 60/270,123
FRIOR FILING DATE: 2001-02-22
FRIOR FILING DATE: 2001-02-22
FRIOR FILING DATE: 2001-02-22
FRIOR FILING DATE: 2001-02-22
FRIOR FILING DATE: 2001-03-22
FRIOR F
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APPLICANT: COLE, S.T.

TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR TITLE OF INVENTION: COMPARATIVE MYCOBACTERIOSES.

TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR TITLE OF INVENTION: TREATHENT OF MYCOBACTERIOSES.

FILE REPERBENCE: 03495,0218

CURRENT APPLICATION NUMBER: US,10/080,170

PRIOR PILLING DATE: 2002-06-10

PRIOR PILLING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 652

SOFTWARE: PACEULIN Ver. 2.1

ENGTHARE: PACEULIN Ver. 2.1
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; Publication No. US20030129601A1
; GENERAL INFORMATION:
    APPLICATION COLE S.T.
    TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
    TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
    TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
    CURRENT APPLICATION NUMBER: US/10/080,170
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Pred. No. 40;
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Pred. No. 40;
0; Mismatches 2; Indels
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; ORGANISM: Mycobacterium leprae
US-10-080-170-155
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; ORGANISM: Mycobacterium leprae
US-10-468-356-155
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Best Local Similarity 77.8
Matches 7; Conservative
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_107390C.1.pep
US-10-424-599-151015
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LOCATION: (1)..(275)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                 ; Sequence 153774, Application US/10437963 ; Publication No. US20040123343A1 ; GENERAL INFORMATION:
                                            83.8%;
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Best Local Similarity 77.8
East Local Similarity 77.8
                                         Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                    1 GVAAXSSLF
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US-10-437-963-153774
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LENGTH: 250
US-10-468-356-538
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Publication No. US20040197896A1;
Publication No. US20040197896A1;
Publication No. US20040197896A1;
APPLICANT: COLE, STEWART
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENEOMICS AS A TOOL FOR TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES;
FILE REFERENCE: 05394.0019;
CURRENT APPLICATION NUMBER: US/10/468,356
CURRENT APPLICATION NUMBER: US/08-19;
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR APPLICATION NUMBER: 2001-02-22;
NUMBER OF SEQ ID NOS: 655
SEQ ID NO S: 655
LENGTH 167
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US-10-060-170-538

US-10-060-170-538

Squence 538, Application US/10080170

Publication No. US20040121322A9

GENERAL INFORMATION:

TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR

TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR

TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES

FILE REFERENCE: 03495.0218

CURRENT APPLICATION NUMBER: US/10/080,170

CURRENT FILING DATE: 2002-06-10

PRIOR FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 652

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 538
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                                                                                                                                                               TYPE: PRT ; CRGANISM: Mycobacterium tuberculosis US-10-080-170-538
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US-10-080-170-538
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ORGANISM: Mycobacterium tuberculosis
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION WUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 652
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 538
LENGTH: 167
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Best Local Similarity 77.8
Matches 7; Conservative
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US-10-468-356-538
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APPLICANT: La Rosa, Thomas J.
APPLICANT: APPLICANT: Covalic, David K.
APPLICANT: APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-2163221.)
CURRENT PELING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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Publication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 151015
LENGTH: 275
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Score 31; DB 17; Length 167;
Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT4530_S3698C.1.pep
US-10-437-963-153774
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APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PELING DATE: 2003-02-20
FRIOR PILING DATE: 2000-03-21
FRIOR PILING DATE: 2000-03-26
FRIOR PELING DATE: 2000-03-26
FRIOR FILING DATE: 2000-03-26
FRIOR PLILNG DATE: 2000-03-26
FRIOR FILING DATE: 2000-03-26
FRIOR PLILNG DATE: 2000-03-06
FRIOR PLILNG DATE: 2000-03-06
FRIOR APPLICATION NUMBER: 60/230,335
FRIOR PILING DATE: 2000-03-09
FRIOR PLILNG DATE: 2000-10-23
FRIOR PELING DATE: 2000-11-23
FRIOR PLILNG DATE: 2000-11-27
FRIOR PLILNG DATE: 2000-11-27
FRIOR PLILNG DATE: 2000-11-27
FRIOR APPLICATION NUMBER: 60/263,625
FRIOR APPLICATION NUMBER: 60/263,636
FRIOR APPLICATION NUMBER: 60/263,636
FRIOR PLILNG DATE: 2001-12-22
FRIOR APPLICATION NUMBER: 60/263,308
FRIOR PLILNG DATE: 2001-02-09
FRIOR FILING DATE: 2001-02-06
FRIOR FILING DATE: 2001-02-16
FRIOR PADE FILING DATE: 2001-02-16
FRIOR FILING DATE: 2001-02-17
FRIOR FILING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 30; DB 15; Length 367;
Pred. No. 1.6e+02;
1; Mismatches 2; Indels
                    Sequence 57719, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAMBKKEY: MISC FEATURE
LOCATION: (32) ... (32)
OTHER INFORMATION: X=any amino acid
US-10-282-122A-57719
                                                                                                        APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Tawick, John
APPLICANT: Tawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Enterococcus faecium
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Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                         Sequence 46362. Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: US/10/767,701
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63126
SEQ ID NO 46362
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                       83.8%; Score 31; DB 15; Length 275; 77.8%; Pred. No. 70; 2; Indels ive 0; Mismatches 2; Indels
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Pred. No. 81;
0; Mismatches 1; Indels
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Pred. No. 89;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Clone ID: SORBI-28MAY03-C17501_1.pep
US-10-767-701-46362
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US-10-767-701-37015
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87.5%;
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Best Local Similarity 77.8%;
Matches 7; Conservative
Query Match
Best Local Similarity 77.0.
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Best Local Similarity 87.5
Matches 7; Conservative
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ORGANISM: Sorghum bicolor
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ORGANISM: Sorghum bicolor
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US-10-767-701-37015
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Sequence 2, Application US/10267756
Publication No. US20030235811A1
GENERAL INFORMATION:
APPLICANT: Redinbo, Matthew
APPLICANT: Sompop, Bencharit
APPLICANT: Potter, Philip
APPLICANT: Morton, Christopher
TITLE OF INVENTION: EMPLOYING SAME

RESULT 13

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Gaps ; 0

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Publication No. US20020077453A1
GENERAL INFORMATION:
APPLICANT: Mayville, Patricia
APPLICANT: Beavis, Ronald
APPLICANT: Beavis, Ronald
APPLICANT: Devision Novel Staphylococcus Perildes For BACTERIAL
TITLE OF INVENTION: INTERFERENCE
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION NUMBER: US/10/032,950
CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR PILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 9
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NAME/KEY: VARIANT
LOCATION: (5)
OTHER INFORMATION: Xaa represents any amino acid at this position. US-10-032-950-1
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FILE REFERENCE: Attorney Docket No. US20030235811A1 421-63-2
CURRENT APPLICATION NUMBER: US/10/267,756
CURRENT FILING DATE: 2002-10-09
FRIOR APPLICATION NUMBER: 60/374,513
FRIOR FILING DATE: 2002-04-22
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.0
ISRUTH: 565
TYPE: PRI
CRAMICH: 565
TYPE: 5
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 GVALLSSLF 256
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US-10-032-950-1
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Search completed: October 26, 2004, 16:10:11 Job time : 32.5 secs

1 GVNAXSSLF 9

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October 26, 2004, 15:46:55; Search time 8.73529 Seconds (without alignments) 99.132 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                      283416
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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37
1 GVAAXSSLF 9
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

De		~~	hypothetical prote	, ,	Ή,		hypo	conserved hypothet	-14	carboxylesterase (hypothetical prote	Н	a bic	ase C -	AgrD protein [impo	hetical	2		sfuA protein precu	probable iron-bind	iron(III)-binding	NADH2 dehydrogenas	NADH2 dehydrogenas	fructose-bisphosph	0	6)	å	ATP c	carrier
ίΩ	H10F30	99000	980	24	004	T43566	B83602	AC2730	D97511	A29923	E64399	F85056	C69224	151291	C89995	T15556	D82756	S33223	QRSEUA	T43918	AH0359	T12291	T12290	ADRBA	ADHUA	ADMSA	ADRIA	'n	S17917
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Score	3.3	, ,	1 E	31	30	30	30	30	30	30	29	29	29	28	28	28	28	28	28	. 58	28	28	28	28	28	28	28	28	28
Result No.		4 0	a m	4	ιΛ	9	7	80	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	20

ADP, ATP carrier pr	ADP, ATP carrier pr	ADP, ATP carrier pr	MFS permease [impo	probable transport	manganese transpor	hydroxymethylpyrim	probable thiamin b	hypothetical prote	hypothetical prote	hypothetical prote	protein K07F5.12a	hypothetical prote	hypothetical prote	hypothetical prote	transposase alr850
S21974	S16568	S14876	AH2859	F97636	AF2539	T07834	E86363	T23422	T23420	T23424	B88:794	AB1251	T46711	B38116	AC2563
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386	387	387	396	396	442	523	525	545	612	638	981	182	184	188	188
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75	75	7.5	7.5	75	7.5	75	7.5	75	75	7.5	75	73	73	73	7.
28	28	28	28	28	28	78	28	28	28	28	28	27	27	27	27
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 T18528 probable pyruvate (flavodoxin) dehydrogenase (EC 1.2.99) - Giardia intestinalis NyAlternate names: pyruvate:ferredoxin oxidoreductase C.Species: Giardia intestinalia
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004 C;Accession: T18528
R;Townson, S.M.; Hanson, G.R.; Upcroft, J.A.; Upcroft, P. Eur. J. Biochem. 220, 439-446, 1994
A;Title: A purified ferredoxin from Giardia duodenalis. A;Reference number: S42359; MUID:94170792; PMID:8125101
A;Status: T18528 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule Lype: DNA A;Sesidues: 1-1253 <tom> A;Cross-references: UNIPROT:Q24982; EMBL:L27221; NID:9960281; PID:9960283; PIDN:AAA7489</tom>
Query Match 89.2%; Score 33; DB 2; Length 1253; Best Local Similarity 77.8%; Pred. No. 19; Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GVAAXSSLF 9
Db 906 GIAACSSLF 914
RESULT 2
conserved hypothetical protein ML1255 [imported] - Mycobacterium leprae C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004 C;Accession: A87066
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; H.R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd
A; Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S. A; Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002 A;Accession: A87066 A:Status: preliminary
A; Molecule type: DNA A; Residues: 1-163 <sto></sto>
A;Cross-references: UNIPROT:Q9CC58; GB:AL450380; NID:g13093193; PIDN:CAC31636.1; GSPDB:CC;Genetics:
A;Gene: ML1255 C;Superfamily: Mycobacterium leprae hypothetical protein MLCB1610.16

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A;Gene: yscJ
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B83602
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                                                                                                                                                                                                       hypothetical protein Rv2468c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Ju1-1998 #sequence_revision 17-Ju1-1998 #text_change 09-Ju1-2004
C;Accession: C7086
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajantream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C7086
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Cross-references: UNIPROT:053195; GB:AL021246; GB:AL123456; NID:93261507; PIDN:CAAL604
A;Cross-references: UNIPROT:053195; GB:AL021246; GB:AL123456; NID:93261507; PIDN:CAAL604
C;Genetics:
A;Gene: Rv2468c
C;Superfamily: Mycobacterium leprae hypothetical protein MLCB1610.16
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virC-region lipoprotein yscJ (YlpB) - Yersinia enterocolitica plasmid pYV
C;Species: Yersinia enterocolitica
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Score 31; DB 2; Length 163; Pred. No. 7.7; 0; Mismatches 2; Indels
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Pred. No. 7.9;
0; Mismatches 2; Indels
  83.8%; Score 31; 77.8%; Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 83.8%;
Best Local Similarity 77.8%;
Matches 7; Conservative
                                         Conservative
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                                                                                                                     132 GVAAASSAF 140
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Best Local Similarity
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C;Date: 21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change 09-Jul-2004
C;Accession: A40049
R;Michiels, T.; Vanooteghem, J.C.; Lambert de Rouvzoit, C.; China, B.; Gustin, A.; Boudr
J. Bacteriol. 173, 4994-5009, 1991
A;Title: Analysis of virC, an operon involved in the secretion of Yop proteins by Yersin, A;Reference number: A40049
A;Accession preliminary
A;Molecule type: DNA
A;Residues: J-244 cMIC>
A;Acsassion: Analysis of virC, an operon involved in the secretion of Yop proteins by Yersin, A;Residues: preliminary
A;Molecule type: DNA
A;Residues: J-244 cMIC>
A;Genetics:
C;Genetics:
A;Genome: plasmid
C;Superfamily: invasin secretion factor mxiJ
C;Keywords: lipid binding; lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43566; T42861
C;Accession: T43566; T42861
B;Hu, P.; Elliott, J.; McCready, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; Brubaker, J. Bacteriol. 180, 5192-5202, 1998
J; Bacteriol. 180, 5192-5202, 1998
A;Afille: Structural organization of virulence-associated plasmids of Versinia pestis.
A;Reference number: 222578; MUID:984224, PMID:9748454
A;Accession: T43566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Experimental source: strain KIM reherston, J.D.; Rose, D.J.; Gregor, J.; Blattner, F.R. Ferry, R.D.; Straley, S.C.; Fetherston, J.D.; Rose, D.J.; Gregor, J.; Blattner, F.R. mfect. Immun. 66, 4611-4623, 1998 in the low-Ca2+-response plasmid pcDl of Yersinia p. Fittle: DNA sequencing and analysis of the low-Ca2+-response plasmid pcDl of Yersinia p. Reference number: 222273; MJID:98427122; PMID:9746557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Residues: 1-244 <HUP>
Cross-references: UNIPROT:Q00926; EMBL:AP053946; NID:g2996222; PIDN:AAC62607.1; PID:g2
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A.Experimental source: strain KIM5
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Pred. No. 20;
2; Mismatches
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C, Superfamily: invasin secretion factor mxiJ
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Best Local Similarity 66.7%;
Matches 6; Conservative
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143 GVAASASVF 151
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Best Local Similarity
Matches 6; Conserv
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A; Residues: 1-244 < PER>
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C;Genetics

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carboxylesterase (EC 3.1.1.1), TCCD-induced 60K microsomal - rabbit Cispecies: Oryctolagus cuniculus (domestic rabbit)
Cipate: 08-Dec-1988 #sequence_revision 08-Dec-1988 #text_change 09-Jul-2004
CiAccession: A29923; A29471
R;Korza, G.; Ozols, J.
R;Korza, G.; Ozols, J.
Biol. Chem. 263; 3486-3495, 1988
A;Title: Complete covalent structure of 60-kba esterase isolated from 2,3,7,8-tetrachlos A;Reference number: A29923; MUID:88139431; PMID:3343253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein MJ0797 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: E£4399
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R; Rirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A. rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschi A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: E64399
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q58207; GB:U67524; GB:L77117; NID:g2826321; PIDN:AAB98792.1
C;Genetics:
A;Map position: FOR720661-721764
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Biol. Chem. 262, 15316-15321, 1987

A;Title: Isolation and characterization of a 60-kilodalton glycoprotein esterase from 1:
A;Reference number: A29471; MUID:88033124; PMID:3667634
A;Accession: A29471

A;Molecule type: protein
A;Residues: 1-71,193-208,436-446;532-539 <0200
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C;Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein
F;32-S26/Domain: cholinesterase homology <CHE>
F;61.363/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;195,441/Active site: Ser, His #status experimental
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Pred. No. 50;
0; Mismatches
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87.5%; Pred. No. 24;
iive 0; Mismatches
                                         A, Gene: AGR C_2304
A, Map position: circular chromosome
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Best Local Similarity 87.5%;
Matches 7; Conservative (
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Best Local Similarity
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.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-267 <STO>
A;Residues: 1-270 <ASTO>
A;Experimental source: strain PAO1
A;Experimental source: strain PAO1
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C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Accession: AC2730
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I. K;Wood, D.W.; Setubal, J.C.; Kaul, R.; Morker, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-305 cKUR>
A;Kesidues: 1-305 cKUR>
A;Cross-references: UNIPROT: Q8UFZ6; GB:AE008688; PIDN:AAL42257.1; PID:g17739654; GSPDB:GA;Experimental source: strain CS8 (Dupont)
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A,Residues: 1-305 <KUR>
A,Genetics: C)Genetics: UNIPROT:Q8UFZ6; GB:AE007869; PIDN:AAK87045.1; PID:g15156295; GSPDB:G
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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24;
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Best Local Similarity 87.5%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.1%; Score 30; DB 66.7%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Gene: PA0340
C,Superfamily: hypothetical protein HI0902
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A, Map position: circular chromosome
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Best Local Similarity 66.7
Matches 6; Conservative
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219 GIAATSMLF 227
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C; Genetics:

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Search completed: October 26, 2004, 16:06:07
Job time: 9.73529 secs
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C89995
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C69214
C69214
cobalamin biosynthesis protein N - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: C69224
R;Shitch, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Ciu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;References: 1-1668 ATH->
A;Cross-references: UNIPROT:027011; GB:AE000868; GB:AE000666; NID:g2622025; PIDN:AABBS542
A;Experimental source: strain Delta H
                                                                                                                                                                       hypothetical protein AT4g04480 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: F85056
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617158
A;Accession: F85056
A;Accession: F85056
A;Accession: P85056
A;Accession: P85056
A;Accession: P85056
A;Cross-references: UNIPROT:Q9XEC5, GB:NC_001268; NID:g7267205; PIDN:CAB77916.1; GSPDB:G
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151291
aldolase C - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: on. 151291
R;Meighan-Mantha, R.L.; Tolan, D.R.
J. Cell. Biochem. 57, 423-431, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Start codon: GTG
C;Superfamily: Methanobacterium thermoautotrophicum cobalamin biosynthesis
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Pred. No. 2.2e+02;
1; Mismatches 2; Indels
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Pred. No. 54;
2; Mismatches
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Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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1273 GIAAISRLF 1281
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                                         GVAAISSL 34
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1 GVAAXSSL 8
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A,Gene: AT4g04480
A,Map position: 4
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A, Title: Noncoordinate changes in the steady-state mRNA expressed from aldolase A and al A; Reference number: 151291; MUID:95286677; PMID:7768978
A, Accession: 151291
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 1-42 - MEIP
A, Stestences: UNIPROT:092007; GB:S78288; NID:9999389; PIDN:AAB34479.1; PID:9999390; C; Superfamily: fructose-bisphosphate aldolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AgrD protein [imported] - Staphylococcus aureus (strain N315)
(Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: C89995
E;Kuroda, M.; Ohta, T.; Uchiyama, I.; Paba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
Ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: UNIPROT:033586; GB:BA000018; PID:g13701831; PIDN:BAB43124.1; GSPDB:G
Experimental source: strain N315
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                                                                                                                                                                                                                                                                             Score 28; DB 2;
Pred. No. 11;
0; Mismatches
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ilarity 77.8%; Pred. No. 12;
Conservative 0; Mismatches
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Best Local Similarity 66.7
Matches 6; Conservative
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Matches 7; Conserv
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-47 <KUR>
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October 26, 2004, 15:44:50; Search time 40.6324 Seconds (without alignments) 127.445 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                        OM protein - protein search, using sw model
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37
1 GVAAXSSLF 9
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Perfect score:
Sequence:
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1825181 seqs, 575374646 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Q836b5 enterococcu Q7ulx9 rhodopirell	Q8sva3 encephalito Q87jd9 vibrio para	Q98g45 rhizobium l Q7mqz7 wolinella s		Q9n4sl caenorhabdi	Q9xec5 arabidopsis	Q9hkz8 thermoplasm	Q979s9 thermoplasm	Q7msa0 wolinella s	Q7kra2 drosophila	Aas64847 drosophil
Q836B5 Q7ULX9	Q8SVA3 Q87JD9	Q98G45 Q7MQZ7	Y797 METJA	Q9N4S1	Q9XEC5	Q9HKZ8	636160	Q7MSA0	Q7KRA2	AAS64847
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ALIGNMENTS

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Zue	PRELIMINARY;	22,	22,		protein Osonbaou NBa0011L09.21;	(japonica cultiv	iridiplantae, Sti	a; Magnoliophyta;	e; Oryzeae; Oryza 1947.		1 N.A.	fuan Q., Ouyang s	.ь., Bera J.J.,	H., Zismann V.,	Ouackenbush J.	IL-2001) to the I		N.A.		4Y-2002) to the P	1 N.A.	omosome 10 Sequer	ew of structure,		1566-1569(2003).	4	Vina R.A., McComb	4Y-2003) to the F	38; AAM22720.1; -				3006186; T phtase	9; Metallophos; 1				91	//.8%; vative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olsen G.J., Sogin M.L.,
"Draft sequence of the Giardia lamblia genome.";
submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.
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GO; GO: 0016491; F:iron ion binding; IEA.

RO; GO: 0016491; F:iron ion binding; IEA.

RINCEPRO; IPR001869; POR.

R InterPro; IPR001869; POR.

R InterPro; IPR001869; POR.

R Pfam; PF01859; POR.

R Pfam; PF01859; POR.

R Pfam; PF01859; POR.

R Pfam; PF01859; POR.

R PF1875; PR00187; TPP_GORY.

R PRINTS; PR00187; TPP_GORY.

R PRINTS; PR001861; GP485RPDOXIN.

R PROSITE; PS00189; 4FE45RPEDOXIN.

R PROSITE; PS00189; 4FE45RPEDOXIN.

R PROSITE; PS001867; CP485E2; UNKNOWN.

R PROSITE; PS001867; CP485E2; PATES PF85856419C9 CRC64;
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Pred. No. 1.1e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                GLP 159 16450 19713.
Glardía lamblía ATCC 50803.
Bukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
NCBI_TaxID=184922;
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Glardia lamblia (Glardia intestinalis).

Bukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
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Upcroft P., Healey A., Upcroft J., Townson S.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=94170792; PubMed=8125101;
Townson S.M., Hanson G.R., Upcroft J.A., Upcroft P.;
Tay purified ferredoxin from Giardia duodenalis.";
Bur. J. Biochem. 220:439-446 (1994).
                                                                                                                                                                                           01-MAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                 PRT; 1087 AA
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Best Local Similarity 77...
7; Conservative
                                                                                                                                 PRELIMINARY;
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Q7QZK4;
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EMBL, ALS90445; CAD26577.1; -.

EMBL, ALS90445; C.Membrane, 1.

GO; GO:00060279; F:amino acid-polyamine transporter activity; IEA.

GO; GO:0006865; P:amino acid transport; IEA.

InterPro: IRROQ422; AA/rel_permease2.

Pfam; PFIO1490; Aa_trans; 1.

ERQUENCE 385 AA; 43605 MW; OEEB01706C82ECAE CRC64;
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Nature 414:450-453(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Fungi, Microsporidia, Unikaryonidae, Encephalitozoon.
NCBI_TaxID=6035;
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R EMBL; L27221; AAA74894.1; -.
R PIR; T18528; T18528.
R GO; GO:0005489; Fielectron transporter activity; IEA.
GO; GO:0005806; Fielectron transporter activity; IEA.
GO; GO:0006189; Fielectron transport; IEA.
GO; GO:0006189; Fielectron transport; IEA.
R GO; GO:0006189; Pielectron transport; IEA.
R InterPro; IPR001450; FPR04 feed; ferredoxin.
R InterPro; IPR002869; POR.
R InterPro; IPR002869; POR.
R InterPro; IPR00389; POR.N.
R InterPro; IPR003919; POR.N.
R Pfam; PF01559; POR.N; 1.
R Pfam; PF01559; POR.N; 1.
R Pfam; PF01559; POR.N; 1.
R PRINTS; PR00353; FE44; Z.
R PRINTS; PR00359; AFF45 FERREDOXIN.
R PROSITE; PS00199; AFF45 FERREDOXIN.
R PROSITE; PS00199; AFF45 FERREDOXIN.
R PROSITE; PS00199; AFF45 FERREDOXIN.
R PROSITE; PS00198; AFF45 FERREDOXIN.
W 4F6-45; Iron; Iron-sulfur; Metal-binding; Pyruvate.
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Pred. No. 1.2e+02;
1; Mismatches 1; Indels
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01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Putative AMINOACID TRANSPORTER.
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Best Local Similarity 77.5
Best Local Similarity 77.5
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374 GVAAFASLF 382

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MEDLINE=22608306; PubMed=12692562;
Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;
Sakaki Y., Hattori M., Omura S.;
"Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitiis.";
Mat. Biotechnol. 21:226-531(2003).
EMBL; APO05027; BAC69394.1; -
Complete proteome; Hypothetical protein.
SEQUENCE 391 AA, 42006 MW, B3BD8F2F27CAE3D8 CRC64;
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Galagan J.E., Calvo S.E., Borkovich K.A., Selker B.U., Read N.D.,
Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.
Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
Selitrennikoff C.P., Kinsey U.A., Braun E.L., Zelter A., Schulte U.
Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.
Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
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Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21477403; PubMed=11572948;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                           Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Last sequence update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                  Streptomycineae; Streptomycetaceae; Streptomyces.
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Pred. No. 70;
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                                                                                                                  01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                          Hypothetical protein.
OrderedLocusNames=SAV1683;
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Best Local Similarity 77.0.
1. Conservative
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                                                          PRELIMINARY;
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SEQUENCE FROM N.A.
STRAIN=MA-4680;
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Name=NCU09316.1;
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                                                                                              D82MH7;
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Q7SDF5
RESULT 5
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NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Bacteria; Actinobacteria; Actinobacteriums; Corymbacterineae; Mycobacterium; Corymbacterineae; Mycobacterium; Mycobacterium; Mycobacterium avium complex (MAC).
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                                                                                                                                                                                                                                                                                                                                                                                              Length 788;
                                                                                                                                                                                                                                                                                                                                                                                              86.5%; Score 32; DB 2; Length 788
77.8%; Pred. No. 1.4e+02;
.ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32; DB 2; Length 128
Pred. No. 2.2e+02;
1; Mismatches 1; Indels
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1289 AA; 143051 MW; D97EC15A661BE3BD CRC64;
                                                                                                                                                                                                                                                                                            preliminary data.
EMBL; AABX01000055; EAA34784.1; -.
SEQUENCE 788 AA; 83602 MW; FE558C3E25E31E5A CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
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EMBL; AAAB01008986; EAA00365.1;
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Best Local Similarity //...
7; Conservative
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Name=ebiG8849; ORFN
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Q7PZ77
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Nature 393:537-544 (1998).
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053195
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                                                           Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V., Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AE017235, AAS04605.1; -
Complete protecome; Hypothetical protein.
SEQUENCE 158 AA; 16266 MW; 2B63DC649F12A95B CRC64;
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EMBL, ABOLJ235, AASO4605.1; -.
HYpotherical protein.
SEQUENCE 158 AA, 16266 MW, 2B63DC649F12A95B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium paratuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1770;
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Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1769;
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02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Mil255.
OrderedLocusNames=Mil255;
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Best Local Similarity 77.6-
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Best Local Similarity 77.8'
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AAS04605;
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T.,
Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Kregn A., McLean J., Moule S.,
Murphy L.D., Oliver S., Seeger K., Kregn A., McLean J., Moule S.,
Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares
Sulston J.B., Taylor K., Mhitchead S., Barrell B.G.,
Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
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STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=10. Eisen J.A., Carpenter L., White O.,
Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,
Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,
Fraser C.M.;
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Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
Barrell B.G.;
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053195, Q7D735,
01-UUN-1998 (TERMELrel. 06, Last sequence update)
01-UUN-1998 (TERMELrel. 06, Last sequence update)
01-OCT-2004 (TERMELrel. 28, Last annotation update)
Hypothetical protein MT2543.
Mycobacterian tuberculosis.
Mycobacterian tuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corymebacterineae, Mycobacterium.
NCBL TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                       83.8%; Score 31; DB 2; Length 163; 77.8%; Pred. No. 52; indels ive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                Complete proteome, Hypothetical protein.
SEQUENCE 163 AA; 16842 MW; F26A1A2C04E3FD2E CRC64;
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SEQUENCE 167 AA, 17288 NW, F600B6FCA54E4BB4 CRC64,
                                                                    "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
EMBL; AA563921. CAC31636.1; -.
Leproma, ML1255; -.
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EMBL, BX642579; CAAL6045.1; -.
EMBL, AE007091; AAK46843.1; -.
PIR; C70866; C70866.
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Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative C
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Best Local Similarity 77.8
Matches 7; Conservative
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Q9LE76;
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Eiglmeier K., Honore N., Woods S.A., Caudron B., Cole S.T.;
"Use of an ordered cosmid library to deduce the genomic organization
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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James K.D., Parklil J., Barrell B.G., Rajandream M.A.;
James K.D., Parklil J., Barrell B.G., Rajandream M.A.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AL049913; CAB43162.1; -.
PIR; T45243; T45243.
Hypothetical protein.
SEQUENCE 169 AA; 17360 MW; 2FB50C9E845D0B89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seeger K.J., Harris D.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                           01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
10-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypotheitcal protein Mb2495c.
OrderedLocusNames=Mb2495c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9X7B5;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
Hypothetical protein MLCB1610.16.
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                                                                                                                                                            167 AA
                                                                                                                                                            PRT;
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Mol. Microbiol. 7:197-206(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 77.00
Section 7, Conservative
                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 GVAAASSAF 144
                                 GVAAASSAF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GVAAXSSLF 9
                                                                                                                                                                                                                                                                                                                                                   Mycobacterium bovis.
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                                                                                                                                                                                                                                                                                                                                                                                                                            MCBI_TaxID=1765;
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Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,

N. W.J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,

N. Hosokawa S., Maeukawa M., Ariwawa Y., Chiden Y., Hayashi M.,

Hosokawa S., Hond T., Aoki H., Arita K., Hamada M., Harada C.,

Hijishita S., Honda M., Ichikawa Y., Idohuma A., Iijima M., Ikeda M.,

Ikeno M., Itoh S., Itoh Y., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,

Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,

Nachita K., Machara T., Mizuno H., Mizubayashi T., Mukai Y.,

Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K, Shibata M.,

Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsui K.,

Naki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,

Yano M., Jiang J., Gojobri T.,
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                                                                                                                            Gaps
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
101-0CT-2004 (TrEMBLrel. 28, Last annotation update)
11-0CT-2004 (TrEMBLrel. 28, Last annotation update)
12-0CT-2004 (TrEMBLrel. 28, Last annotation update)
13-0CT-2004 (TrEMBLRel. 28, Last a
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Sukaryota, Virtálplantae; Streptophyta; Bahryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
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Nature 420:312-316(2002).
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Pred. No. 80;
            Length 169;
                                                                                                                      Indels
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Chamba E., Halford N.G., Wilkinson M., Shewry P.R.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ll protein.
255 AA; 26887 MW; 0CA5C39B99987549 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Beta-kafirin precursor.
            5,
Score 31; DB 2
Pred. No. 54;
0; Mismatches
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DR EMBL, AJ717660, CAG30668.1; -.

DR InterPro: IPR0005612; AAI.

DR InterPro: IPR0005612; AAI.

DR InterPro: IPR000480; Gludenin.

DR InterPro: IPR000480; Gludenin.

DR PRINTS; PR002134; Tryp alpha amyl; 1.

DR PRINTS; PR00219; GLTADGLUTEN.

DR SMART; SM00499; AAI; 1.

PT SIGNAL

FT CHAIN

SQ SEQUENCE 191 AA; 20605 MW; A99F952C9E2C311F CRC64;

Query Match

Best Local Similarity 87.5%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps

QY I GVAAXSSL 8

Db 123 GVAAASSL 130
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Search completed: October 26, 2004, 16:04:59 Job time : 43.6324 secs

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GenCore version 5.1.6
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2003bs:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	c	. aureus	grD-auto	yclic pe	Staphyloc	Staphyloc	Peptide-m	Protected	AgrD2 lac		grD2 lin	. aureus	taphyloc	Peptide-m	AgrD2 lac	Protected	AgrD-auto	Cyclic pe	Bacterial	Pimaricin	isease t	Transcrip	eptide-m	AgrD2 thi	. aureus
	Description	Aay67854 S	Aam50902 Ac		0						Aam51002 Ac	മ	ഗ		Aam51005 A	Aam50908 P	_	Abp53540 C	_	Aab31559 P	Adk62934 D	Aaw38323 T	Abb07159 P	Н	Abb84631 S
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SOFTWANTES	ΙD	AAY67854	AAM50902	ABP53543	AAY67860	AAY67859	ABB07160	AAM50907	AAM51004	AAM51003	AAM51002	AAY67851	AAY67861	ABB07161	AAM51005	AAM50908	AAM50899	ABP53540	ADF04608	AAB31559	ADK62934	AAW38323	ABB07159	AAM51001	APR4631
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o k	Query	94.6	94.6	4.	ဖ	φ	ģ	യ	86.5	vo	86.5	ന	83.8	m.	m.	m.	ω.	83.8	m.	83.8	83.8	81.1	81.1	81.1	,
	Score	35	35	32	35	32	32	32	32	32	32	31	31	31	31	31	31	31	31	31	31	30	30	30	3.0
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Adj98875 Peptide t Abb84634 S. aureus Adf09193 S. aureus Ade09086 Novel pro Ade09086 Novel pro Ade09265 Novel pro Ade012 Human tra Aag49535 Arabidops Aag49534 Arabidops Aag49534 Arabidops Aag496057 Novel pro Ade09057 Novel pro	A949533 Arabidops A940453 Arabidops A940453 Arabidops Abb9136 Herbicida Adn74713 Thale cre Ade08283 Novel pro Abg75820 Transport Abg77840 Human sug Add37440 Human tra
ADJ98875 ABB84634 ADB09086 ADB09265 AAB60112 AAG49535 AAG4534 AAG4534	AAG4533 AAG4533 AB991365 ADN'4713 ADE08283 AAG75820 AAU76036 ADD37440
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Query Match
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                                                                                                       Sequence 9
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                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                  ABP53543;
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(NOVI/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of a novel synthetic cyclic peptide of the invention that is capable of inhibiting the agr response of the invention that is capable of inhibiting the agr response of the stability of the sequence aureus. It is an Agrb-autoinduing peptide, where AgrD is a secreted agr-encoded peptide and where the agr locus controls the synthesis of virulence factor and other extracellular proteins for pathogenicity in S. aureus. Preferred peptides may have the sequence NNI2-X(N)-2-X(Y)-cool, with a cyclic bond between the Z cresidue and COOH other than a thiosester bond, where X is an amino acid, an amino acid analogue, a peptidomimetic or non-amide isostere, Z is a namino acid analogue, a peptidomimetic or non-amide isostere, Z is a namino acid analogue, a peptidomimetic or non-amide isostere, Z is a synthetic or a biosynthetic amino acid, n is 0-10 and y is 1-10. The cyclic bond is especially a lactam or lactone bond. The thiololactone structure within native AgrD peptides is required for activation of the cyclic agr response. Blimination of the thiol ester component of the cyclic ring structure can destroy agr response activating activity while preserving and enhancing inhibitory activity. A claimed method of preparing a cyclic
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with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus \,
                                                                                                                                                                                                                                                                                                                                                                                                 note= "note linked to residue 9 to form cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "note linked to residue 5 to form cyclic peptide"
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in a
                                                                                                                                                                                                                                                                                                            Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic; antibacterial; infection; therapy; cyclic.
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                                                                                         0; Indels
                                                              94.6%; Score 35; DB 3; Length 100.0%; Pred. No. 1.7e+06; ive 0; Mismatches 0; Inde
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                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "any amino acid"
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                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novick RP,
                                                                                                                                                                                                       AAMS0902 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0090402P.
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                                               Query Match
Best Local Similarity 100.00
Best Local 9; Conservative
                                                                                                                                                                                                                                                         (first entry)
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                                    Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                  Synthetic
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ID AAM
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peptide involves: assembling a linear peptide chain on to a solid phase resin support; deprotecting the resulting protected assembled peptide; treating the deprotected peptide with neutral buffer for a time sufficient to form the cyclic peptide and cleave the peptide from the support; and recovering the cyclic peptide. The peptide is useful for bacterial interference, especially for the treatment of S. aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP53540 to ABP53547 represent cyclic peptides (1) from the present invention. The present invention also describes a method for treating Staphylococcus aureus infection comprising the administration of a composition comprising (1). (1) has antibacterial activity, and can used as an agr gene response inhibitor. The peptides are useful for
                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                  Length 9;
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                                                                                                                                                                                                                                                94.6%; Score 35; DB 5; Le
llarity 100.0%; Pred. No. 1.7e+06;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP53543 standard; peptide; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treating S. aureus infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-DEC-2001; 2001US-00032950.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cyclic peptide SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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MAYVILLE P.
NOVICK R P.
BEAVIS R.
JI G.
                                                                                                                                                                                                                                                                                                                                                                                1 AVNAXSSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-681366/73
                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                1 AVNAXSSLF
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                                                                                                                                                                                                   AA;
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24-JUN-1999;
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Matches

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AAY67860;

AAY67860

us-10-032-950-4.rag

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This sequence represents the Staphylococcus aureus AgrDII derived peptide. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibite the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus
                                                                                                                                                                                                                                                                                                    New cyclic peptides for treating infections with Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vulnerary; pheromone; agr system; accessory gene regulator; cyclic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide-mediated quorum sensing inhibitor peptide cyclo-XII.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 9;
                                                                                                                                                                                                                                        Beavis R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 3; I
Pred. No. 1.7e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNIV PRINCETON.
QUOREX PHARM INC.
UNIV TECHNOLOGIES INT INC.
                                                                                                                                                                                                                                        Novick RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
ABB07160
ID ABB07160 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                       Example; Page 22; 37pp; English
                                                                                                                         99WO-US014562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 86.5%;
Local Similarity 87.5%;
les 7; Conservative (
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2000US-0254398P
                                                                                                                                                          98US-00103438
                                                                                                                                                                                        (UYRQ ) UNIV ROCKEFELLER.
(UYNY ) UNIV NEW YORK STATE.
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                                                                                                                                                                                                                                        Muir TW, Mayville P,
                              Staphylococcus aureus.
                                                                                                                                                                                                                                                                       WPI; 2000-147202/13.
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virulence factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9 AA;
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07-DEC-2000;
                                                                                                                             24-JUN-1999;
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                                                             WO9967286-A2
                                                                                            29-DEC-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB07160;
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(QUOR-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New cyclic peptides for treating infections with Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
 Gaps
                                                                                                                                                                                                                                                                           Staphylococcus aureus infection; AgrD; agr response; treatment; virulence factor.
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                                                                                                                                                                                                                                       Staphylococcus aureus AgrDII derived peptide sequence.
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 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY67859 standard; peptide; 9 AA.
                                                                                                                                            AAY67860 standard; peptide; 9 AA.
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(UYNY ) UNIV NEW YORK STATE.
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                                                                                                                                                                                                             (first entry
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 Conservative
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                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus.
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Best Local Similarity
Matches 7; Conserr
                                1 AVNAXSSLF
                                                               1 AVNAXSSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9 AA;
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Surette MG;

AAY67859;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "note linked to residue 9 to form cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "note linked to residue 5 to form cyclic peptide"
                             Use of autoinducer-2 agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis, also antibiotic compositions.
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic; antibacterial; infection; therapy; cyclic.
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0
                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                   Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                       Protected peptide used in cyclic peptide production.
                                                                                                                                                                                                                                                  Score 32; DB 5; I
Pred. No. 1.7e+06;
0; Mismatches 1;
                                                                   Disclosure; Page 33; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "Ser(tBu)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "Ser(Bzl)"
                                                                                                                                                                                                                                                                                                                                                             AAM50907 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                  86.5%;
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(UYNY ) UNIV NEW YORK STATE.
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                                                                                                                                                                                                                                       Query Match
Best Local Similarity 87.5.
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note=
          WPI; 2002-075235/10.
                                                                                                                                                                                                                                                                                                            2 VNASSSLF 9
                                                                                                                                                                                                                                                                                         2 VNAXSSLF
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                                                                                                                                                                                                             quorum sensing
                                                                                                                                                                                                                               Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
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The present sequence is that of a protected peptide used in an example of the preparation of novel synthetic cyclic peptides of the invention (see AAMS0899-900). The peptide corresponds to the Staphylooccusa aureus AAMS089-900, The peptide accorresponds to the Staphylooccusa aureus chain assembly, the peptide was cleaved from the support and the Ser-5 caid-anisole:water mixture (90:5:5) for 4 hr. The partially protected peptide-alpha carboxylates were then dissolved in DMF and treated with peptide-alpha caralytic amount of dimethylaminopyridine. Cyclization was complete after 2 hr. The remaining protecting groups were then removed by treatment with HF and the peptide purified by HPLC. The cyclic peptide is capable of inhibiting the agr response of staphylooccus aureus. The thiololactone structure within native AgrD peptides is required for activation of this response. Replacement of the thiol ester component of the cyclic ing structure with a lactone (as in the present case) or a lactam can destroy agr response activating activity while preserving and enhancing inhibitory activity. The cyclic peptides are useful for the cyclic inference, especially for the treatment of S. aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                               Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
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       Beavis R,
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   Novick RP,
                                                                                                                                                                                                                                                                     Disclosure; Col 14; 18pp; English.
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(first entry)
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Best Local Similarity 87.5
Matches 7; Conservative
Mayville P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus.
Synthetic.
                                                                   WPI; 2002-170774/22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9 AA;
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08-MAY-2002
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                                                                                                                                                                                                  subject.
   Muir '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
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98US-0090402P.

24-JUN-1998;

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The present sequence is that of a novel synthetic AgrD2 lactone cyclic peptide in which residue 5 of the peptide is linked to residue 9 via a lactone bond. The peptide is derived from an AgrD2 peptide 9 via a secrete by the factor and stable from an AgrD2 peptide of actorious aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agrs promoter. This allowed activation or inhibition of the agr response to be monitored spectrophotometrically. The lactone AgrD2 peptide inhibited the agr response of group I S. aureus strains without contained cyclic peptides (see AAMG0899-906 and AMG0899-906 and methods for preparing them, especially peptides where the cyclic bond is a lactone bond. The cyclic peptides are useful for bacterial interference, especially for the treatment of S. aureus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
                                                                                                                 Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32; DB 5; I. Pred. No. 1.7e+06; ); Mismatches 1;
                                                          Beavis R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beavis R,
                                                        Novick RP,
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                                                                                                                                                                              Example 1; Col 9; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AgrD2 linear free acid peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.5%;
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(UYNY ) UNIV NEW YORK STATE.
            (UYRQ ) UNIV ROCKEFELLER.
(UYNY ) UNIV NEW YORK STATE.
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Best Local Similarity 87.5-
                                                        Mayville P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus.
Synthetic.
                                                                                     WPI; 2002-170774/22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9 AA;
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                                                       Muir TW,
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                                                                                                                                               subject.
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The present sequence is that of a novel synthetic AgrD2 linear free acid peptide. The peptide is derived from the cyclic AgrD2 peptide of Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agris prometer. This allowed activation or inhibition of the agr response to be monitored spectrophotometrically. Unlike an AgrD2 thiololactone cyclic peptide (see AAM51001), the present peptide was unable to either activate or inhibit the agr response, even when added to cultured cells at um concentrations. The invention provides claimed cyclic peptides (see AAM50899) and methods for preparing them. The cyclic peptides are useful for bacterial interference, especially for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in a subject.
             Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in
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Pred. No. 1.7e+06;
); Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM51002 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                         treatment of S. aureus infection
                                                                         Example 1; Col 9; 18pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AgrD2 linear thioester peptide.
                                                                                                                                                                                                                                                                                                                                                                                    86.5%;
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(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VNASSSLF 9
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VNAXSSLF
                                                                                                                                                                                                                                                                                                                                                        Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM51002;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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The present sequence is that of a novel synthetic AgrD2 linear thioester peptide. The peptide is derived from the cyclic AgrD2 peptide of Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agrP3 promoter. This allowed activation or inhibition of the agr response to be monitored spectropherometrically. Unlike an AgrD2 thiololactone cyclic peptide (see AAM51001), the present peptide was unable to either activate or inhibit the agr response, even when added to cultured cells at un concentrations. The invention provides claimed cyclic peptides (see AAM50999) and methods for preparing them. The cyclic peptides are useful for bacterial interference, especially for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a cyclic peptide derived from the Staphylococcus aureus AgrD peptide. The invention relates to AgrD derived peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New cyclic peptides for treating infections with Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus infection; cyclic peptide; AgrD; agr response; virulence factor; treatment.
                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                    Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S. aureus peptide #1 used for bacterial interference.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beavis R;
                                                                                                                                                                                                                                                                                                                                                    Score 32; DB 5; I
Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ji G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novick RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY67851 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                 treatment of S. aureus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Page 26; 37pp; English.
Example 1; Col 9; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Unknown
                                                                                                                                                                                                                                                                                                                                                      86.5%;
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(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Muir TW, Mayville P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
'-hea 7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                          2 VNAXSSLF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-147202/13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                    Sequence 9 AA;
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AAY67851
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This sequence represents the Staphylococcus aureus AgrDII derived peptide. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus
activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New cyclic peptides for treating infections with Staphylococcus aureus
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus infection; AgrD; agr response; treatment;
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100.0%; Pred. No. 1.7e+06;
ive 0; Mismatches 0; Indels
                                                                                      Length 9;
                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus AgrDII derived peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beavis R;
                                                                                   Score 31; DB 3; Le
Pred. No. 1.7e+06;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ji G,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                           83.8%; Scc.
100.0%; Pred
0; N
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                                                                                                                                                                                                                                               AAY67861 standard; peptide; 9 AA.
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(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mayville P,
                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus
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                                                                                     Ouery Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VNAXSSLF
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                                                                                                                                                2 VNAXSSLF
                                                                                                                                                                                                                                                                                                                                                                             virulence factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9 AA;
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                                                            Sequence 9
                                                                                                                                                                                                                                                                            AAY67861;
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(revised)
(first entry)

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AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection; therapy; cyclic.
                                                                                                                                                                                               Key Location/Qualifiers
Misc-difference 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYRQ ) UNIV ROCKEFELLER.
(UYNY ) UNIV NEW YORK STATE.
                                                            AgrD2 lactam cyclic peptide
                                                                                                                                               Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-170774/22.
                                                                                                                                                                                                                                               Misc-difference 5
                                                                                                                                                                                                                                                                                 Misc-difference
              07-AUG-2003
08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                  24-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUN-1998;
                                                                                                                                                                                                                                                                                                                                  US6337385-B1
                                                                                                                                                                                                                                                                                                                                                                08-JAN-2002.
                                                                                                                                                                 Synthetic
The invention relates to the use of autoinducer-2 (AI-2) agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis. Syncatyistic antibiotic compositions comprising inhibitors of the quorum-sensing pathway of a microorganism are also provided. Methods using such AI-2 analogues are useful for treating pathogen-associated disease states. The compounds and antibiotic compositions can be used to inhibit bacterial cell growth and/or biofilm formation on a medical device, particularly for promoting growth of skin graft replacements used in the treatment of burns and ulcers. They may also be used to aid wound repair, and to inhibit bacterial cell growth and biofilm formation in or on products or devices used for personal hygiene. The present sequence represents a inhibitor of peptide-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of autoinducer-2 agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis, also antibiotic compositions.
                                                                                                                                                                          Autoinducer-2; AI-2; antibiotic, antibacterial, dermatological, vulnerary; pheromone; agr system; accessory gene regulator; cyclic.
                                                                                                                                        Peptide-mediated quorum sensing inhibitor peptide cyclo-XIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stein J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 9;
                                                                                                                                                                                                                                                                                             /note= "diaminoprprionic acid residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.8%; Score 31; DB 5; Le
100.0%; Pred. No. 1.7e+06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shokat K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dammel CS, Schauder S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 33; 134pp; English.
                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYPR-) UNIV PRINCETON.
(QUOR-) QUOREX PHARM INC.
(UYTE-) UNIV TECHNOLOGIES INT INC.
                                          ABB07161 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                               10-MAY-2001; 2001WO-US015221
                                                                                                                                                                                                                                                                                                                                                                                                                               10-MAY-2000; 2000US-0203000P.
                                                                                                          13-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-075235/10.
                                                                                                                                                                                                                                                                                                                               WO200185664-A2
                                                                                                                                                                                                                                                             Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          quorum sensing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bassler BL,
                                                                                                                                                                                                                                                                                                                                                               15-NOV-2001
                                                                                                                                                                                                                             Synthetic
                                                                          ABB07161;
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Ji G;

Beavis R,

/note= "note linked to residue 5 to form cyclic peptide"

note= "any amino acid"

99US-00339511. 98US-0090402P

/note= "note linked to residue 9 to form cyclic peptide"

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The present sequence is that of a novel synthetic AgrD2 lactam cyclic peptide in which residue 5 of the peptide is linked to residue 9 via a lactam bond. The peptide is derived from an AgrD2 peptide 9 via a statam bond. The peptide is derived from an AgrD2 peptide 9 via a staphylococous aureus group II. AgrD2 is a secreted agr-encoded peptide. Staphylococous aureus group II. AgrD2 is a secreted agr-encoded peptide. The synthesis of virulence factor and other where the agr locus controls the synthesis of virulence factor and other biological activity of the synthesic peptide was assayed using cultured 5. aureus strains containing a beta-lactamase reporter gene fused to the agrs promoter. This allowed activation or inhibition of the agr response to be monitored spectrophotometrically. The AgrD3 lactam peptide inhibited the agr response in group I S. aureus strains and did not activate the agr response in group I S. aureus strains and did not provides claimed cyclic peptides (see AAMS0899-906 and AAMS0899-906 and AAMS0899-906 and AAMS0899-906 and AAMSO899-906 and AAMSO899-906 and AAMSO899-906 and AAMSO899-906 and AAMSO899-906 and interference, especially for the treatment of S. aureus infection.

(Updated on 07-AUG-2003 to correct OS field.)
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Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in a
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100:0%; Pred. No. 1.7e+06;
ive 0; Mismatches 0;
                                                                                                                                                             Example 1; Col 11; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM50908 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VNAXSSLF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9 AA;
                                                                              subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
AAM50908
ID AAM50
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Gaps

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0; Indels

AAM51005 standard; peptide; 9 AA.

RESULT 14
AAMS1005
ID AAMS1
XX
AC AAMS1

AAM51005

2 VNAXSSLF 2 VNAXSSLF

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The present sequence is that of a protected peptide used in an example of the preparation of novel synthetic cyclic peptides of the invention (see AM56899-906). The peptide corresponds to the Staphylococcus aureus of AM56899-906. The peptide corresponds to the Staphylococcus aureus of ADTDII sequence with a Cyss to diaminopropionic acid (Dpr) mutation (action strategy. Following chain assembly, the peptide was cleaved from the support and the Dpr-5 residue deprotected by treatment with a trifluoracetic acid:anisole:water mixture (90:5:5) for 4 hr. The partially protected peptide-alpha carboxylates were then dissolved in DMF and treated with Py80P. Cyclization was complete after 2 hr. The remaining protecting groups were removed by treatment with HF and the peptide purified by HPLC. The cyclic peptide is capable of inhibiting the captive AgrD peptides is required for activation of this response. Replacement of the thiol ester component of the cyclic ring structure within a lactam (as in the present case) or a lactone can destroy agr response activating activity while preserving and enhancing inhibitory activity. The cyclic peptides are useful for becterial interference, especially for the treatment of S. aureus infection
                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUN-1999;
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                                        08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                     US6337385-B1
                                                                                                                                                                                                                                                                                                                                                                                                08-JAN-2002.
                                                                                                                                        Synthetic
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Gaps

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Query Match 83.8%; Score 31; DB 5; Length 9; Best Local Similarity 100.0%; Pred. No. 1.7e+06; Matches 8; Conservative 0; Mismatches 0; Indels

Sequence 9 AA;

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to residue 9 to form cyclic peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in a
                                                                                                                                         Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic; antibacterial; infection; therapy; cyclic.
                                                                                           Protected peptide used in cyclic peptide production.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muir TW, Mayville P, Novick RP, Beavis R,
                                                                                                                                                                                                                                                                                                                                                                 'note= "note linked
                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Col 14; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "Ser(Bzl)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "Ser(Bzl)"
                                                                                                                                                                                                                                                                                                                                                                                                                   label = Dpr (Boc)
                                                                                                                                                                                                                                                                                                                     note= "Z-Gly"
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(UYNY ) UNIV NEW YORK STATE.
                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-170774/22.
                                                                                                                                                                                                                                                                                                                                            Misc-difference
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                                                                                                                                                                                                                                                                    Key
Modified-site
AAM50908;
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2 VNAXSSLF
     2 VNAXSSLF
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Search completed: October 26, 2004, 15:59:42 Job time : 43.75 secs \cdot

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Wed Oct 27 09:38:12 2004
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October 26, 2004, 15:54:00 ; Search time 31.5 Seconds (without alignments) 92.502 Million cell updates/sec
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1: /cgn2_6/prodate/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/prodate/2/pubpaa/PCT7_BW PUB.pep:*
3: /cgn2_6/prodate/2/pubpaa/PCT7_BW PUB.pep:*
4: /cgn2_6/prodate/2/pubpaa/USO6_NEW PUB.pep:*
5: /cgn2_6/prodate/2/pubpaa/USO6_NEW PUB.pep:*
6: /cgn2_6/prodate/2/pubpaa/USO7_NEW PUB.pep:*
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19: /cgn2_6/prodate/2/pubpaa/USIOP_PUBCOMB.pep:*
10: /cgn2_6/prodate/2/pubpaa/USIOP_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1364641 seqs, 323758627 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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37
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                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 4, Appli	Sequence 6225, Ap	Sequence 1, Appli	Sequence 3, Appli	Sequence 6, Appli	Sequence 206201,	Sequence 44650, A	Sequence 46660, A	Sequence 64168, A	Sequence 174739,	Sequence 168046,	Sequence 151317,	Sequence 2, Appli
SUMMARIES	ID	US-10-032-950-4	US-10-369-493-6225	US-10-032-950-1	US-10-201-444-3	US-10-201-444-6	US-10-424-599-206201	US-10-767-701-44650	US-10-767-701-46660	US-10-425-114-64168	US-10-437-963-174739	US-10-424-599-168046	US-10-437-963-151317	US-09-919-781-2
	DB	13	14	13	14	14	15	16	16	15	16	15	16	σ
	* Query Match Length DB	6	633	ov	თ	47	130	140	265	298	303	343	538	572
,	* Query Match	94.6	91.9	83.8	81.1	81.1	81.1	81.1	81.1	81.1	81.1	81.1	81.1	81.1
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ALIGNMENTS

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US-10-032-950-4
; Sequence 4, Application US/10032950;
; Sequence 4, Application US/20020077453A1
; Sequence 4, Application No. US20020077453A1
; GENERAL INFORMATION:
A PPLICANT: Maryille, Patricia
A PPLICANT: May US20020077453A1ick, Richard P.
A PPLICANT: May US20020077453A1ick, Richard P.
A PPLICANT: Beavis, Ronald
A PPLICANT: Ji, Guangyong
IITLE OF INVENTION: UNTERPRENCE
FILE OF INVENTION: UNTERPRENCE
FILE REPERRINCE 600-1-231M
CURRENT APPLICATION NUMBER: US/10/032,950
FILE REPERRINCE: 000-1-231M
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SEQ ID NOS: 8
SEQ ID NOS: 8
SEQ ID NO 4
FILE RIFER NECRATION: Description of Artificial Sequence
FEATURE: PATURE: PATURE INFORMATION: Deptide
FEATURE: OTHER INFORMATION: Deptide
MAME/KES: VARLANT
COTHER INFORMATION: Axa represents any amino acid at this position.
US-10-032-950-4
OURLY MATCH
Best Local Similarity 100.0%; Pred. No. 1.28+06;
Matches 9; Conservative 0, Masmatches 0; Indels 0; Gaps
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1 AVNAXSSLF 9

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APPLICANT: LA ROSA Thomas J
APPLICANT: LA ROVALIC David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
                                                                                                                                                                   Publication No. US20030078378A1

Sequence 3, Application US/10201444

Publication No. US20030078378A1

GENERAL INFORMATION:

TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
FILE REPERENCE: 63753/7

CURRENT APPLICATION NUMBER: US/10/201,444

CURRENT PILING DATE: 2002-07-23

PRIOR PAPLICATION NUMBER: US/08/861,476

PRIOR FILING DATE: 1997-05-22

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin version 3.0

LENGTH: 9

LENGTH: 9
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GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION:

FILE REPERENCE: 6.375.3/7

CURRENT FILING DATE: 1997-62.2

PRIOR APPLICANT: NOWBER: US/08/861,476

PRIOR APPLICANT: 1997-05-22

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin version 3.0

SEQ ID NO 6

SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81.1%; Score 30; DB 14; Length 47; 87.5%; Pred. No. 22; 1; Indels iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 87.5%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-201-444-6
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Best Local Similarity 87.5
....has 7; Conservative
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2 UNAXSSLF
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US-10-201-444-3
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                                                                                                           US-10-369-493-6225

Sequence 6225, Application US/10369493

Fublication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Garden V. Yongwei
APPLICANT: Glaman, Barry S.
APPLICANT: Glaman, Barry S.
APPLICANT: Glaman, Barry S.
APPLICANT: Chen, Xianfeng TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFERIES
FILE REFERENCE: 38-10 (52052)B
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SECOTOR: FRIENDED FOR THE CONTROL OF THE CONT
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; Sequence 1, Application US/10012950
; Publication No. US20020077453A1
; GENERAL INCOMMATION:
; APPLICANT: Mayville, Patricia
; APPLICANT: Mayville, Patricia
; APPLICANT: Beavis, Ronald
; APPLICANT: Beavis, Ronald
; TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; TITLE OF INVENTION: NUMBER: US/10/032,950
; TITLE OF INVENTION NUMBER: US/10/032,950
; FILE REFERENCE: 60/00-1-231N
; CURRENT PAPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PATENTIN VEY: 2.0
; SEQ ID NO 1
; LENGTH: DATE: PATENTIN VEY: 2.0
; SEQ ID NO 1
; LENGTH: PATENTIN VEY: 2.0
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NAME/KEX: VARIANT
LOCATION: (5)
OTHER INFORMATION: Xaa represents any amino acid at this position. US-10-032-950-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Caenorhabditis elegans US-10-369-493-6225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
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ORGANISM: Artificial Sequence
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   1 AVNAXSSLF 9
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US-10-032-950-1
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2 VNAXSSLF 9

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ORGANISM: Sorghum bicolor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 44650, Application US/10767701
Sequence 44650, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Acovalic, David K.
APPLICANT: Cahou, Yihua
APPLICANT: Cahou, Yought
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
CURRENT FILING DATE: 2004-01-29
CURRENT FILING DATE: 2004-01-29
SEQ ID NO 44650
LENGTH: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 46660, Application US/10767701

Sequence 46660, Application US/10767701

Publication No. US20040172684A1

GENERAL INFORMATION:

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 46660
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                                                                                                                                                                                                                                                                                                                                                                       81.1%; Score 30; DB 15; Length 130; 66.7%; Pred. No. 64; 2; Indels tive 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT3847_28226C.1.pep
US-10-424-599-206201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C740_1.pep
US-10-767-701-44650
                                                                                                                                                                                                          NAME/KEY: unsure
LOCATION: (1)..(130)
CHER INFORMATION: unsure at all Xaa locations
FEATURE:
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FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 206201
LENGTH: 130
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Best Local Similarity 66.
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Best Local Similarity 66.7
Matches 6; Conservative
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ORGANISM: Sorghum bicolor
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127 AINAIKSLF 135
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                                                                                                                                        TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AVNAXSSLF 9
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US-10-437-963-174739

// Sequence 174739, Application US/10437963

// Sequence 174739, Application US/10437963

// Sequence 174739, Application US/10437963

// Publication No. US20040123343A1

// REPLICANT: LA ROSA, Thomas J.

// APPLICANT: Exovalic, David K.

// APPLICANT: Cao, Yongwei

// APPLICANT: Boukharov, Andrey A.

// APPLICANT: Barbazuk, Brad

// APPLICANT: Barbazuk, Brad

// APPLICANT: Li, Ping

// TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

// TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

// TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

// TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

// TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

// CURRENT APPLICATION NUMBER: US/10/437,963

// CURRENT FILING DATE: 2003-05-14

// WUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 64168, Application US/10425114
Publication No. US2C040034888A1
GENERAL INFORMATION
APPLICANT: Liu, Unadong
APPLICANT: Zhou, Yihua
APPLICANT: Tabaska, Jack E
APPLICANT: TILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRESENCE: 38-21 (5313)8
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 64168
IENGTH: 298
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                                                                                                          Length 265
                                                                                                        Score 30; DB 16; Length 26
Pred. No. 1.4e+02;
0; Mismatches 2; Indels
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FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C104_77.pep
US-10-767-701-46660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: LIB3593-001-E12_FLI.pep
US-10-425-114-64168
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66.7%; Pred. No. 1.5e+02;
tive 1; Mismatches 2;
                                                                                                          81.1%;
                                                                                                        Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                   17 AVNVPSSLF 25
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hes 6; Conserv
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ORGANISM: Zea mays
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US-10-425-114-64168
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LENGTH: 303
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RESULT 14
US-10-154-419-13

Sequence 13, Application US/1015419

Publication No. US20030143675A1

GENERAL INFORMATION:
APPLICANT: Outris, Rory A.J.
APPLICANT: Glucksman, Maria Alexandra
APPLICANT: Meyers, Rachel 1

TITLE OF INVENTION: 67076, 67102, 44181, 67084EL, 67084ALT, FBH58295FL, 57255, TITLE OF INVENTION: AND 57259, 67102, 44181, 67084ALT, FBH58295FL, 57255, TITLE OF INVENTION: AND 5725alt MOLECULES AND USES THEREFOR
FILE REFERENCE: MNI-249

CURRENT APPLICATION NUMBER: US/10/154,419

CURRENT APPLICATION THOUGH SEQUENCE: NUMBER OF SEQ ID NOS: 99

SOFTWARE: FSECSEQ Version 4.0

SEQ ID NO 13

LENGTH: 572
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Sequence 2, Application US/09919781

Sequence 2, Application US/09919781

GENERAL INFORMATION:

APPLICANT: CULTES, ROY A.J.

TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF

TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/919, 781

CURRENT APPLICATION NUMBER: US/09/919, 781

PRIOR PRILING DATE: 2000-07-31

NUMBER OF SEQ ID NOS: 3

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 572
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                        Score 30; DB 16; Length 538;
Pred. No. 2.9e+02;
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Pred. No. 3.1e+02;
1; Mismatches 1; Indels
                                                                                                0; Mismatches
                            81.1%;
77.8%;
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Best Local Similarity 77.8%;
Matches 7; Conservative
                            Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                            328 APNASSSLF 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
US-09-919-781-2
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ORGANISM: Homo sapiens
                                                                                                                                                                1 AVNAXSSLF 9
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US-09-919-781-2
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; Publication No. US2040123343A1
; Publication No. US2040123343A1
; Publication No. US2040123343A1
; Publication No. US2040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Bradd
; APPLICANT: Bradd
; APPLICANT: Bradd
; APPLICANT: All Pands and Uses Thereof for Plant Improvement
; TILLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TILLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TILLE OF INVENTION: Solution NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 151317
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 168046, Application US/10424599
Fublication No. US20046031072A1
GENERAL INFORMATION:
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Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels
                                                            81.1%; Score 30; DB 16; Length 303;
66.7%; Pred. No. 1.6e+02;
tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT3847_122761C.1.pep
US-10-424-599-168046
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COTHER INFORMATION: Clone ID: PAT_MRT4530_51471C.1.pep
US-10-437-963-151317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1)...(343)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                            Best Local Similarity 66.7
Matches 6; Conservative
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290 AINAIKSLF 298
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ORGANISM: Oryza sativa
                                                                                                                                                                                                   1 AVNAXSSLF 9
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                   US-10-424-599-168046
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US-10-437-963-151317
US-10-437-963-174739
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                                                                Query Match
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RESULT 15

US-10-424-599-196029

US-10-424-599-196029

Squence 196029, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Kovalic David K

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPRENENCE: 38-21(3)223) B

CURRENT FILING DATE: 2003-04-28

CURRENT FILING DATE: 2003-04-28

NOMBER OF SEQ ID NOS: 285684

SEQ ID NO 196029
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81.1%; Score 30; DB 15; Length 832;
Best Local Similarity 77.8%; Pred. No. 4.6e+02;
Matches 7; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: unsure
COCATION: (1)...(832)
CHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_1903C.1.pep
US-10-424-599-196029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AVNAXSSLF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
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Search completed: October 26, 2004, 16:10:12 Job time : 32.5 secs

387 AVNPFSSLF 395

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October 26, 2004, 15:46:55; Search time 8.73529 Seconds (without alignments) 99.132 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                  283416
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                              283416 segs, 96216763 residues
                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                     US-10-032-950-4
37
1 AVNAXSSLF 9
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1: Pirl:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                     Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                                                                                                            Searched:
                                                                                                      Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	hypothetical prote	hypothetical prote	N-carbamoy1-beta-a	n-carbamov1-beta-a	c	1:0	æ	ч	aminopeptidase (EC	ase	hypothetical prote	ᇤ	P2B/LAMP-1 precurs	120K lysosomal mem	cholesterol oxidas	DNA topoisomerase	DNA gyrase, chain	DNA gyrase subunit	alpha-mannosidase	hydroxymethylgluta	probable short-cha	dehydrogenase/redu	hypothetical prote	ferrichrome ABC tr	hypothetical prote	DNA-directed DNA p	hypothetical prote		de
												_			_	_														
5	А	T27215	T31617	AH2933	G98348	848463	C89995	813098	A96597	T30943	T30942	F90350	A28067	A60534	A30200	A32260	D70104	C72043	H86579	T30525	A30239	H98193	AB3093	AH2082	C69812	S57145	A81343	T26894	T46291	122
	DB	2	7	7	7	N	α	~	0	N	7	7	0	~	~	7	0	7	~	~	~	N	N	α		N	N	~	~	7
:	Length	633	2055	413	441	926	47	265	315	1016	0	271	382	405	407	546	599	602	602	\circ	1054	273	273	292	333	497	1200	16	195	EO.
æ	ery	; ;	•	ë.	ω.	ë.	ä			81.1		78.4	æ	78.4	78.4	78.4	78.4	78.4	78.4	78.4	78.4									73.0
	Score	34	32	31	31	31	30	30	30	30	30	29	29	29	29	29	29	29	29	29	50	28	28	28	28	28	28	27	27	27
	Result No.		7	m	4	ស	9	7	80	6	10	11	12	13	14	15	16	17	18	13	20	21	22	23	24	25	56	27	28	59

cobalamin adenosyl	probable endonucle conserved hypothet	hypothetical prote	hypothetical prote	glycerol kinase -	probable 3-ketoacy	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	conserved hypothet	non-motile and pha	histidine protein	glutamyl aminopept	probable homeotic
AH1575	B9/225 E99233	AB2215	876029	F70339	D96779	T33320	T27578	T15810	T38683	E83610	A87557	S27533	A47531	A38437
0.0	7 74	~	~	7	~	7	7	•	•	•	6		7	67
251	301	368	375	49,	541	570	573	726	756	760	842	842	95,	99
73.0	73.0	73.0	73.0	73.0	73.0	73.0	73.0	73.0	73.0	73.0	73.0	73.0	73.0	73.0
27	27	27	27	27	27	27	27	27	27	27	27	27	27	27
30	35	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

hypothetical protein	57G11C.1 - Caenorhabditis elegans
C; Species: Caenorhabd	C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #	C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C, Accession: T27215	
submitted to the EMBL	Data Library. September 1997
A; Reference number: Z20330	0330
A, Status: preliminary	A;Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA A; Residues: 1-633 <wil></wil>	
A, Cross-references: U	A; Cross-references: UNIPROT:018227; EMBL: Z99281; PIDN: CAB16503.1; GSPDB: GN00022; CESP:Y
C;Genetics:	
A, Gene: CESP:Y57G11C.1	
A; Map position: 4 A:Introps: 70/1: 329/3	
C; Superfamily: multidrug	ug resistance protein; ATP-binding cassette homology
Query Match	91.9%; Score 34; DB 2; Length 633;
Matches 7; Conse	//.8%; Fred. NO. vative 1; Mismato
Qy 1 AVNAXSSLF	6. <u>-</u>
	——————————————————————————————————————
RESULT 2	
T31617	
nypornerical procein x50E8A.m - C C;Species: Caenorhabditis elegans	bursa.m - caenornabditis elegans tis elegans
C;Date: 29-Oct-1999 #8	C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
Risteward, C.	
submitted to the EMBL	submitted to the EMBL Data Library, September 1999
A; kererence number: 2.	
A; Status: preliminary; translated	translated from GB/EMBL/DDBJ
A; Molecule type: DNA A: Residues: 1-2055 < WIL->	
A; Cross-references: EN	A;Cross-references: EMBL:AL117200; NID:e1549770; PIDN:CAB55056.1; CESP:Y50E8A.m
A; Experimental source: clone Y50E8A	clone Y50E8A
A; Introns: 273/3: 447/1:	1: 526/1: 735/1: 1247/1: 14:8/1: 1494/1: 1753/3
Query Match	86.5%; Score 32;
7;	//.of; vative 1

1751 ALNAFSSLF 1759

1 AVNAXSSLF 9

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Cybers: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
Cybersion: 849463
Rybowman, Cytherer, C.
submitted to the EMBL Data Library, September 1994
A,Reference number: 548455
A,Accession: 848463
A,Accession: 1-926 < BOW>
A,Acces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: MRNA
A;Residues: 1-265 < VURA
A;Cross-references: UNIPROT: P27497; EMBL:XS5892; NID:g22354; PIDN:CAA39376.1; PID:g22355
C;Superfamily: chlorophyll a/b-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agrophotein [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision.10-May-2001 #text_change 09-Jul-2004
C;Accession: C89995
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
R;Kuroda, M.; Ohta, T.; Mobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C; Shiba, T.; Hattcri, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Hitle: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Accession: S13098
R;Viret, U.F.; Schantz, M.L.; Schantz, R.
Nucleic Acids Res. 18, 7179, 1990
A;Title: Nucleotide sequence of a maize cDNA coding for a light-harvesting chlorophyll a A;Reference number: S13098; WUID:91088340; PMID:2263499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:033586; GB:BA000018; PID:g13701831; PIDN:BAB43124.1; GSPDB:G
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Description: involved in endoplamic reticulum to Golgi transport; required for vesicle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
Species: Saccharomyces cerevisiae
Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chlorophyll a/b-binding protein precursor - maize
C;Species: Zea mays (maize)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 30; DB 2; Length 47;
Pred. No. 2;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C, Genetics:
A, Gene. SGD: SEC24; SEC24; MIPS: YIL109c
A, Cross-references: MIPS: YIL109c; SGD: S001371
C, Function: 9L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.1%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|| |||
787 INATSSLF 794
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Molecule type: DNA
Residues: 1-47 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ster, E.W.

A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Status: preliminary

A;Molecule type: DNA

A;Molecule type: DNA

A;Residues: 1-413 <KUR>
A;Cross-references: UNIPROT:Q8UBE6, GB:AE008689; PIDN:AAL43886.1; PID:g17741433; GSPDB:G

A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 n-carbamoyl-beta-alanine amidohydrolase PA0444 [imported] - Agrobacterium tumefaciens (s C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004 C;Accession: G98348 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: AH2933
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, I Rerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Accession: G98348
A,Status: preliminary
A,Molecule type: DNA
A,Rolacule type: LNA
A,Rolacule type: LNA
A,Cross-references: UNIPROT:Q8UBE6; GB:AE007870; PIDN:AAK90313.1; PID:g15160344; GSPDB:(C,Genetics:
                                                                                                                                                                                                                                                                                                                                     N-carbamoyl-beta-alanine amidohydrolase [imported] - Agrobacterium tumefaciens (strain C,Species: Agrobacterium tumefaciens C,Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carbamoyl-beta-alanine amidohydrolase PA0444 [imported] - Agrobacterium tumefaciens Species: Agrobacterium tumefaciens Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 31; DB 2; Length 413;
Pred. No. 13;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Map position: linear chromosome .
C,Superfamily: N-carbamyl-L-amino acid amidohydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: AGR L 3478
A;Map position: linear chromosome
C;Superfamily: N-carbamyl-L-amino acid amidohydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
848463
SEC24 protein - yeast (Saccharomyces cerevisiae)
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83.8%; 77.8%;

Query Match Best Local Similarity 77.0 ----- 7; Conservative

C,Genetics: A,Gene: amaB

ઠે

274 AVNALGSLF 282

g

1 AVNAXSSLF 9

Local Similarity hes 7; Conserv

Query Match Best Local S Matches 7

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mainopeptidase (EC 3.4.11.-) - Indian meal moth
C;Species: Plodia interpunctella (Indian meal moth)
C;Species: Plodia interpunctella (Indian meal moth)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: T30942
R;Zhu, Y.C.; Oppert, B.; Kramer, K.J.; McGaughey, W.H.; Dowdy, A.K.
R;Zhu, Y.C.; Oppert, B.; Kramer, K.J.; McGaughey, W.H.; Dowdy, A.K.
A;Description: Molecular comparison of aminopeptidase cDNAs and gene structure between the A;Reference number: 220442
A;Accession: T30942
A;Accession: T30942
A;Residues: 1-1016 < ZHNA
Cross-references: UNIPROT:017484; EMBL:AF034483; NID:g2645992; PID:g2645993; PIDN:AAC:C;Superfamily: membrane alanyl aminopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyberoman membrane gryptocar mouse;
Cybecdes: Mus musculus (house mouse)
Cybecdes: Musculus (house mouse)
Cybecdes: Musculus (house mouse)
Cybecdes: Musculus (house)
Cybe
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A,Residues: 1-271 «KUR»
A,Cross-references: UNIPROT:Q97X81; GB:AE006641; NID:g13815127; PIDN:AAK42061.1; GSPDB:
C,Genetics:
A,Gene: SSO1873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein SSO1873 (imported) - Sulfolobus solfataricus C.Species: Sulfolobus solfataricus C.Species: Sulfolobus solfataricus C.Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004 C.Accession: P90350 C.Accession: P90350 C.A.S., Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; CharJong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. A. Peng, X.; Thi-Ngoc, H.P.; Redder, Arbescription: Sulfolobus solfataricus complete genome. A.Accession: F90350
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2; Mismatches
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2; Mismatches
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66.7%;
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Best Local Similarity 66.7
Matches 6; Conservative
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152 AVNATSALY 160
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C;Species: Plodia interpunctella (Indian meal moth)
C;Accession: T30943
R;Zhu, Y.C.; Oppert, B.; Kramer, K.J.; McGaughay, W.H.; Dowdy, A.K.
Bibmitted to the EMBL Data Library, November 1997
A;Peference number: Z20942
A;Accession: T30943
A;Accession: T30943
A;Status: preliminary
A;Mclaus: preliminary
A;Residues: 1-1016 < ZHNA
A;Cross-references: UNIPROT:017485; EMBL:AF034484; NID:g2645994; PID:g2645995; PIDN:AAC3
C;Superfamily: membrane alanyl aminopeptidase
C;Keywords: aminopeptidase
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C; Keywords: chloroplast; thylakoid; transmembrane protein
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nes 7; Conservative
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152 AVNATSALY 160
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A/Status: Dreliminary
A/Molecule type: DNA
A/Residues: 'V', 2-546 <ISH>
A/Residues: 'V', 2-546 <ISH>
A/Cross-references: UNIPROT: P12676; GB:M31939; GB:J03356; NID:g153210; PIDN:AAA26719.1;
A/Cross-references: UNIPROT: P12676; GB:M31939; GB:J03356; NID:g153210; PIDN:AAA26719.1;
A/Residues: V', 2-546 <ISH
A/Cross-references: UNIPROT: P12676; GB:M31939; GB:J03356; NID:g153210; PIDN:AAA26719.1;
A/Referrit, M.; Ishizaki, T.; Paik, 'S.Y.; Manome, T.; Murcoka, Y.
J. Bacteriol. 172, 3444-3453, 1990
A/Ritler: An operon containing the genes for cholesterol oxidase and a cytochrome P-450-1
A/Reference number: S15809; MUID:90299781; PMID:2361941
                                                                                                                                                                                                                                                                                  A;Title: Nucleotide sequence of the gene for cholesterol oxidase from a Streptomyces sp. A;Reference number: A32260; MUID:89123081; PMID:2914858
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A; Residues: 1-30 (HORA
A; Residues: 1-30 (HORA
A; Residues: 1-30 (HORA
A; Residues: DABL: M31939; GB:J03356; NID:g153210
B; Purcell, J.P.; Greenplate, J.T.; Jennings, M.G.; Ryerse, J.S.; Pershing, J.C.; Sims, M5 Cohem. Biophys. Res. Commun. 196, 1406-1413, 1993
A; Title: Cholesterol oxidase: a potent insecticidal protein active against boll weevil A; Reference number: PC2002; MUID:94071904; PMID:8250897
                                                                                                                                           ;Species: Streptomyces sp.
jbate: 20.0ct-1989 #sequence revision 20-0ct-2000 #text_change 09-Jul-2004
;Accession: A32260; SiSBIO; FC2002
;Ishizaki, T.; Hirayama, N.; Shinkawa, H.; Nimi, O.; Murooka, Y.
Bacteriol. 171, 596-601, 1989
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                                                                                                    cholesterol oxidase (EC 1.1.3.6) precursor [validated] - Streptomyces sp.
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F;43-546/Product: cholesterol oxidase #status experimental <MAT>
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A;Residues: 'XXXTF',48-54,'XX',57,'X',59-60 <PUR>
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P2B/LAMP-1 precursor - mouse
P2B/LAMP-1 precursor - mouse
C;Species: Mrs musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: A60534
C;Accession: A60534
Cancer Res. 49, 6077-6084, 1989
A;Title: Molecular characterization of P2B/LAMP-1, a major protein target of a metastasi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Molecule type: mRNA
A, Residues: 1-407 < HOM's
A, Cross-recences: UNPROT:P14562; EMBL:J03672
A, Note: the authors translated the codon GGG for residue 15 as Val
R; Himeno, M.; Noguchi, Y.; Sasaki, H.; Tanaka, Y.; Furuno, K.; Kono, A.; Sakaki, Y.; Kat
EBES Lett. 244, 351-356, 1989
A, Title: Isolation and sequencing of a cDNA clone encoding 107 kDa sialoglycoprotein in
A, Reference number: S03331; MUID:89153580; PMID:2920835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RiHowe, C.L.; Granger, B.L.; Hull, M.; Green, S.A.; Gabel, C.A.; Helenius, A.; Mellman, Proc. Natl. Acad. Sci. U.S.A. 85, 7577-7581, 1988
A;Title: Derived protein sequence, oligosaccharides, and membrane insertion of the 120-k
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120K lysosomal membrane glycoprotein precursor - rat
NyAlternate names: sialoglycoprotein
C;Species: Rattus norvegicus (Norway rat)
C;Species: 18-Oct-1389 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
                                                                         Gaps
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      78.4%; Score 29; DB 2; Length 382; 75.0%; Pred. No. 36; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.4%; Score 29; DB 2; Length 405; 75.0%; Pred. No. 39; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A30200; MUID:89017240; PMID:3174652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-405 -- LEMEPA
A;Cross-references: UNLFAPOT:P11438
C;Superfamily: lysosome-associated membrane protein
                                                                         Conservative
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257 MNASSSLF 264
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Best Local Similarity
6; Conserve
                                                                                                                                    2 VNAXSSLF 9
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Query Match
Best Local Similarity
Matches 6; Conserv
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à g ô

A; Molecule type: mRNA A; Residues: 22-407 < HIM> A; Residues: 22-407 < HIM> A; Crose-references: EMBL:X14765; NID: 956577; PIDN: CAA32873.1; PID: 956578 A; Note: part of this sequence, including the amino end of the mature protein, was confir C; Superfamily: 1yeosome-associated membrane protein C; Keywords: 91ycoprotein; membrane protein F; 22-407/ Product: 1ysosomal membrane glycoprotein, 107K #status experimental < MAT>

A,Accession: S03331

glycoproteins.

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Gaps

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Length 407; 1; Indels

Score 29; DB 2; Pred. No. 39; 1; Mismatches

78.4%;

Best Local Similarity 75.0 Matches 6; Conservative

Query Match

282 MNATSLF 289

2 VNAXSSLF 9

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plodia inte
shewanella
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arabidopsis
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mus musculu
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sulfolobus
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Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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Last annotation update)
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                                                                                                                                                                                                                                                          ALIGNMENTS
                                            Q8GX26
017484
017485
08EFG6
Q92ZT9
Q9KJP3
Q9KJP3
Q9KJP3
Q9KJP3
Q9VV81
Q9VV81
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Q9DCI3
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                 Q9C780
Q9AT39
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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01-JAN-1998 (TrEMBLrel. 05, Creai
01-JAN-1998 (TrEMBLrel. 05, Last
01-OCT-2003 (TrEMBLrel. 25, Last
Hypothetical protein Y57G11C.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        investigating biology.";
Science 282:2012-2018(1998)
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1 AVNAXSSLF 9
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Matches 7; Conserv
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 Query Match
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018227
8
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Q9cw96 streptomyce
Q75b16 ashbya gos
Aas51681 ashbya gos
P40482 saccharcmyc
033586 staphylococ
Q7a2n4 staphylococ
Cae92745 staphyloc
Cae92751 staphyloc
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Cae92751 staphyloc
Cae92754 staphyloc
Cae32757 staphyloc
Cae32757 staphyloc
Q223149 oryza sativ
Q32214 coprimus ci
Q6yv56 oryza sativ
Q3Cxv56 oryza sativ
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Q9zvu6 arabidopsis
Q61y75 oryza sativ
Q81972 arabidopsis
Q94bs2 arabidopsis
Bac84586 oryza sat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O6t2c4 streptomyce
Aar16516 streptomy
Q9u275 caenorhabdi
O8ube6 agrobacteri
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                                                                                                           October 26, 2004, 15:44:50; Search time 40.6324 Seconds (without alignments) 127.445 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                            1825181
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                             1825181 segs, 575374646 residues
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AAS51681
SC24_YEAST
O33586
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Maximum Match 100%
Listing first 45 summaries
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PROB STRIR
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CAD23149
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Q6YV56
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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1 AVNAXSSLF 9
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Perfect score:
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Result

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RESULT 2
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WormPep; Y50E9A.16; CE24404.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.

GO; GO:0000166; F:nucleotide binding; IEA.

GO; GO:0006810; P:transport; IEA.
                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
                                                                                                                                                                                                                                                                                                          "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPRO11527; ABC_membrane_1.
InterPro; IPRO11527; ABC_membrane_1.
InterPro; IPRO11527; ABC_membrane_1.
InterPro; IPRO1140; ABC_TM transpt.
InterPro; IPRO04439; ABC_Transporter.
Pfam; PF00664; ABC_membrane; 1.
PRO317E; PS00035; AAR_TRANSPORTER_1; 1.
PROSITE; PS00211; ABC_TRANSPORTER_2; 1.
PROSITE; PS00221; ABC_TRANSPORTER_2; 1.
PROSITE; PS00833; ABC_TRANSPORTER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the BMBL/GenBank/DDBJ database EMBL; ALL17200; CAB60586.1; -. HSSP; Q03518: 1.1.77
                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 25, Last annotation update)
Hypotheital protein Y50E8A.16.
Name=Y50E9A.16;
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01-UJN-2002 (TrEMBLrel. 21, Created)
01-UJN-2002 (TrEMBLrel. 21, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
N-carbamcyl-beta-alanine amidohydrolase.
Name=amaB; OrderedLocusNames=Atu3070;
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                     807 AA.
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                     PRT;
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MEDLINE=21608550; PubMed=11743193;
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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                     PRELIMINARY;
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 Q9U275
ID Q9U275
AC Q9U275;
DT 01-MAY-2000 (7
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28 UBB 6
1D 08 UBB 1D
DT 01-JU
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OS Bact
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                     Streptomyces diastaticus.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1956;
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Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycineae, Streptomycetaceae; Streptomyces.
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Pred. No. 75;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                            Seconomics E.M., Perez-Zuniga F.J., Malpartida F.; Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases. BMBL, A444225, ARRISE16.1; -. InterPro; IPR000172; GMC_OXTEG. InterPro; IPR00172; GMC_OXTEG. InterPro; IPR01409; Tat_signal seq; 1. SEQUENCE 599.63, GMC_OXED.1; I SEQUENCE 549 AA, S9306 WW; 7719FSD7D47D0683 CRC64;
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Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY442225; AAR16516.1; -.
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59306 MW; 7719F5D7D47D0683 CRC64;
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AAR16516;
02-MAR-2004 (TYEMBLYEL 27,
02-MAR-2004 (TYEMBLYEL 27,
02-MAR-2004 (TYEMBLYEL 27,
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Best Local Similarity 77.0
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Best Local Similarity 77.0
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327 AINAFSSLF 335
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RESULT 3
AAR16516
ID AAR1
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MEDLINE=20547809; PubMed=11094342;
MEDLINE=20547809; PubMed=11094342;
Aparicio J.F., Fouces R., Mendes M.V., Olivera N., Martin J.F.;
A complex multienzyme system encoded by five polyketide synthase genes is involved in the biosynthesis of the 26 membered polyene macrolide pimaricin in Streptomyces natalensis.";
EMBL; AJZ78573; CAC20926.1; -.
HSSP; P12676; 1MXT.
                                                                                                                                                                                                                                                                                                                                                              Streptomyces natalensis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
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GO; GO:0066118; P:electron transport; IEA.
InterPro; IPR000172; GWC_oxred.
InterPro; IPR006311; Tat.
ITGRPAMS; TIGR01409; TAT signal seq; 1.
PROSITE; PS00623; GWC_OXFED. 1; T.
SEQUENCE 549 AA; 55475 MW; 96759DE780AC5A82 CRC64;
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomycineae; Streptomycetaceae; Streptomyces
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274 AVNALGSLF 282
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STRAIN=ATCC 10895;
PubMed=15001715;
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01-MAR-2001
01-JUN-2003
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Okutra V.K., Zhou Y., Chen L., Wood G.E., Almaida M.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Esen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland B., Palmieri A.,
Kaymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                         "The genome of the natural genetic engineer Agrobacterium tumefaciens \mathbb{C}58."_j
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OrderedLocusNames=AGR_L_3478;

OrderedLocusNames=AGR_L_3478;

OrderedLocusNames=AGR_L_3478;

OrderedLocusNames=AGR_L_3478;

Bacterial Proteobacteria, Alphaproteobacteria, Rhizobiales;

Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.

NCBL_TaxID=176299;
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PIR, AH2933; AH2933.
PIR, G98348; G98348.
GO; GO:0006277; F:hydrolase activity; IEA.
GO; GO:00062037; F:netallopeptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR010158; Hydantase.
InterPro; IPR002933; Peptidase M20.
Pfam; PF01546; Peptidase M20.
TIGRFAWS; TIGR01879; hydantase; 1.
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InterPro; IPR010158; Hydantase.
InterPro; IPR002933; Peptidase M20.
Pfam, PF01546; Peptidase M20; I.
IGRRAMS; IGR01879; hydantase; I.
SEQUENCE: 441 AA; 47628 MW; 7ADSOCF34F86410F CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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77.8%; Pred. No. 1e+02;
iive 0; Mismatches
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SEQUENCE 413 AA; 44639 MW;
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Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavier A.,
Gaffney T.D., Philippsen P.;
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STRAIN=ATCC 10895;
Voegeli S.E., Brachat S., Dietrich F.S., Lerch A., Gaffney T.,
                                                                                                                                                                                                                                                                                                                                                                                                Ine Ashbya gossypii genome as a tool for mapping the ancient Saccharomyces cerevisiae genome."; Science 304:304-307(2004).
              Length 549;
83.8%; Score 31; DB 2; Length 549
77.8%; Pred. No. 1.38+02; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Philippsen P.; Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
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Last sequence update)
Last annotation update)
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Saccharomycetales; Saccharomycetaceae; Eremothecium
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                                         Conservative
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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01-FEB-1995 (Rel. 31, Last sequence update)
01-077-2004 (Rel. 45, Last annotation update)
Protein transport protein Sec.24 (Abnormal nuclear morphology 1).
Name-SEC24, Synonyms-ANU1; OcceredLocusNames-YLL109C;
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungl; Ascomycota; Saccharomycoties;
                                                                                                                                                                                                                                                                                                                           Ashbya gossypii (Yeast) (Eremothecium gossypii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Eremothecium.
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Voegall S.E., Brachat S., Dietrich F.S., Lerch A., Gaffney
Philippean P.;
Submitted (DEZ. 2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AE016889; AAS51681.1; -.
SEQUENCE 891 AA; 99621 MW; 6633CB9E2E0B707B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83.8%; Score 31; DB 2; Length 891; 75.0%; Pred. No. 2.2e+02; tive 1; Mismatches 1; Indels
                                                                                                                             83.8%; Score 31; DB 2; Length 891; 75.0%; Pred. No. 2.2e+02; ive 1; Mismatches 1; Indels
      AGD; ALC239C; -.
InterPro; IPR007123; Gelsoln.
InterPro; IPR006900; Sec23_helical.
InterPro; IPR006895; Sec23_trunk.
InterPro; IPR006895; Zf.Sec23_Sec24.
Pfam; PF00626; Gelsolin; 1.
Pfam; PF04815; Sec23_helical; 1.
Pfam; PF04811; Sec23_helical; 1.
Pfam; PF04811; Sec23_helical; 1.
Pfam; PF04811; Sec23_trunk; 1.
SEQUENCE 891 AA; 99621 MW; 6633CB9E2E0B707B CRC64;
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23-APR-2004 (TrEMBLrel, 27,
23-APR-2004 (TrEMBLrel, 27,
23-APR-2004 (TrEMBLrel, 27,
EMBL; AE016889; AAS51681.1;
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Best Local Similarity 75.v.
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752 INATSSLF 759
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=S2862 / AB972;
MEDIJNB=9313266; PubMed=9169870;
Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D.,
Chillingworth T., Connor R., Devlin K., Gentles S., Hamiln N.,
Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,
Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,
Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome IX.";
Nature 387:84-87(1997).
                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION.
MEDLINE=20219212; PubMed=10753972;
Peng R., De Antoni A., Gallwitz D.;
"Evidence for overlapping and distinct functions in protein transport of coat protein Sec24p family members.";
J. Biol. Chem. 275:11521-11528(2000).
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Pfam; PF00626, Gelsolin; 1.
Pfam; PF04815; Sec23_trunk; 1.
Pfam; PF04810; zf-Sec3_sec24; 1.
Sfam; PF04810; zf-Sec3_sec24; 1.
3D-structure; EndoplasmIc reticulum; Golgi stack; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sec24p and Iss1p function interchangeably in transport vesicle formation from the endoplasmic reticulum in Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION.
MEDILNE=20177547; PubMed=10712514;
Kurihara T., Hamamoto S., Gimeno R.E., Kaiser C.A., Schekman
Yoshihisa T.;
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Poly-Pro.
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PIR, S48463; S48463.
PDB; 1M2V; X-ray; B=1-926.
PDB; 1PCX; X-ray; A=117-925.
PDB; 1PD0; X-ray; A=117-925.
PDB; 1PD1; X-ray; A=117-925.
GermChine; 133644; A=17-925.
SGD; S0001371; SEC24.
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NCBI_TaxID=4932;
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Gaps
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JG., Beavis R., Novick R.P.;
"Bacterial interference caused by autoinducing peptide variants.";
Science 276:2027-2030(1997).
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Pred. No. 2.3e+02;
1; Mismatches 1; Indels
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
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1D 01-JAN-1998 (TrENBLrel. 05, Lag DT 01-JAN-1998 (TrENBLrel. 05, Lag DT 01-DGT-2004 (TrENBLrel. 28, Lag DT 01-DGT-2004 (TrENBLrel. 28, Lag DT Name-agrD; CS Bacteria; Firmicutes; Bacillale OX NCBI_TAXID=1280; RX NCBI_TAXID=1280; RX NCBI_TAXID=1280; RX NCBI_LNE=97342847; PubMed=919726 RX SCIENCE FROM N.A. RC STRAIN=GC31a-Cp5, GC31b-Cp5, GC SUBLIA ANG17715; CAB92755.1; DR EMBL; ANG17715; CAB92754.1; DR EMBL; ANG17719; CAB92754.1; DR EMBL; AN
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Length 47; 1; Indels

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ilarity 87.5%;
Conservative (
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   EMBL; AP003135; BAB43124.1;
                              InterPro; IPR009229; AgrD. Pfam; PF05931; AgrD; 1. Complete proteome. SEQUENCE 47 AA; 5149 MM
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Best Local Similarity 87.5
Matches 7; Conservative
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BEDLINE-21311952. PubMed=11418146;

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

Sekimizu K., Hirakawa H., Kuhara K., Furuya K., Yoshino C., Shiba 'Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

"Whole genome sequencing of meticillin-resistant Staphylococcus
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Bacteria: Firmicutes; Bacillales; Staphylococcus.
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87.5%; Pred. No. 18; ive 0; Mismatches
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Best Local Similarity 87.5%;
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                                                                                                                                                                                                                                                                                                                                           STRAIN=gt3la-cp5;
Goerke C., Dasbach S., Kuemmel M., Wolz C.;
Goerke C., Dasbach S., Kuemmel M., Wolz C.;
and cap in Staphylococcus aureus.";
submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ617715; CAB2745.1;
SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-gt31b-cp5;
Goerke C., Dasbach S., Kuemmel M., Wolz C.;
Goorke C., Dasbach S., Kuemmel M., Wolz C.;
Goory C.,
Evolutionary Models for the Development of the Polymorphic Loci agr and cap in Staphylococcus aureus.";
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJG17716; CAB22748 11. -.
SEQUENCE 47 AA, 5149 MM; 22893764DFS4BFA7 CRC64;
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0; Mismatches 1; Indels
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Last annotation update)
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01-APR-2004 (TrEMBLrel. 27, Last sequence update)
01-APR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
                                                                                                                                                                                               Staphylococcus aureus.
Bacteria: Firmicutes; Bacillales; Staphylococcus.
47 AA.
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op QQ

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October 26, 2004, 15:44:15; Search time 42.75 Seconds (without alignments) 75.522 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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39
1 GVNAXASLF 9
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Perfect score:
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geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Aay67855 S. aureus	_	_	_	_	_	907	4		N	٠,	-	۳,	S	Aam50908 Protected	σ	0	m	Abb07159 Peptide-m	Н	Abb84631 S. aureus	9190	Adj98875 Peptide t	1634 S	Adf09193 S. aureus
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SUMMARIES			AAY67855	50903	ABP53544	AAY67860	67859	ABB07160	AAM50907	51004	AAM51003	AAM51002	57851	57861	ABB07161	AAM51005	AAM50908	AAM50899		AAW38323	07159	AAM51001	34631 .	ADF09190	98875	34634	09193
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Abu44321 Protein e	Adh11546 Chimpanze	Aay67856 S. aureus	Aam50904 AgrD-auto	Abp53545 Cyclic pe	•	Aay67852 S. aureus	Aam50900 AgrD-auto	-		Abp34694 Human ORF	Adc95277 E. faeciu	Abu25396 Protein e	Abu24755 Protein e	Abu35191 Protein e	Adc87185 Human GPC	Adc87445 Human GPC	Abo79302 Pseudomon	Abo78813 Pseudomon	Abg13082 Novel hum
5 ABU44321	7 ADH11546	3 AAY67856	5 AAM50904	5 ABP53545	3 ADN36926	3 AAY67852	5 AAM50900		3 AAB41086	5 ABP34694	7 ADC95277	5 ABU25396	5 ABU24755	5 ABU35191	7 ADC87185	7 ADC87445	7 ABO79302	7 ABO78813	4 ABG13082
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82.1	82.1	79.5	79.5	79.5	79.5	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	6.9
32	32	31	31	31	31	30	30	30	30	30	30	30	30	30	30	30	30	30	30
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 23Sep04:*

Database :

 $\tilde{\Lambda}$ note= "N-terminal residue forms bond with C-terminal residue to form a cyclic peptide" Staphylococcus aureus infection; cyclic peptide; AgrD; agr response; virulence factor; treatment. aureus peptide #5 used for bacterial interference. Location/Qualifiers AAY67855 standard; peptide; 9 AA /label= Unknown 99WO-US014562 98US-00103438. (UYRQ) UNIV ROCKEFELLER. (UYNY) UNIV NEW YORK STATE. (first entry) Staphylococcus aureus. Misc-difference Key Modified-site 24-JUN-1999; 24-JUN-1998; WO9967286-A2 25-APR-2000 29-DEC-1999. AAY67855; AAY67855

Beavis R; Ji G, Muir TW, Mayville P, Novick RP,

WPI; 2000-147202/13.

New cyclic peptides for treating infections with Staphylococcus aureus.

Claim 9; Page 26; 37pp; English.

This sequence represents a cyclic peptide derived from the Staphylococcus aurens AgrD peptide. The invention relates to AgrD derived peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes

us-10-032-950-5.rag

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MUIR T W.
MAYVILLE P.
NOVICK R P.
BEAVIS R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-681366/73
                                                                                                                Query Match
Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
                                                                                                                                                                1 GVNAXASLF
                                                                                                                                                                                     GVNAXASLF
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                                                                                           Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUN-1998;
24-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MUIR/) MUIR
(MAYV/) MAYVI
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                                                                                                                                                                                                                                                                                              13-DEC-2002
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                                                                      infection
                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                        ABP53544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NOVI/)
(BEAV/)
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ABP53544
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                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is that of a novel synthetic cyclic peptide of the invention that is capable of inhibiting the agr response of the stably lococus aureus. It is an AgrD-autoinduing peptide, where AgrD is steplylococus aureus. It is an AgrD-autoinduing peptide, where AgrD is synthesis of virulence factor and where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. Preferred peptides may have the sequence NH2-X(N)-Z-X(Y)-COCH, with a cyclic bond between the Z residue and COOH other than a thiosester bond, where X is an amino acid analogue, a peptidomimetic or non-amide isostere, Z is a namno acid analogue, a peptidomimetic or non-amide isostere, Z is a synthetic or a biosynthetic amino acid, n is 0-10 and y is 1-10. The cyclic bond is especially a lactam or lactone bond. The thiololactone structure within native AgrD peptides is required for activation of the cyclic bond destroy agr response activating activity while preserving and enhancing inhibitory activity. A claimed method of preparing a cyclic
                                                                                 ö
with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus
                                                                                                                                                                                                                                                                                                                                                                    'note= "note linked to residue 9 to form cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "note linked to residue 5 to form cyclic peptide"
                                                                                 Gaps
                                                                                                                                                                                                                                                                                 aureus; AgrD; agr response; inhibitor; antibiotic; infection; therapy; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in
                                                                                 ;
                                                                                                                                                                                                                                                              AgrD-autoinducing cyclic peptide, inhibitor of agr response.
                                                                                0; Indels
                                                        Similarity 100.0%; Pred. No. 1.7e+06; 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                            "any amino acid"
                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novick RP,
                                                                                                                                                                                         AAM50903 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Col 19; 18pp; English
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(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                             'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muir TW, Mayville P,
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                                                                                                         1 GVNAXASLF
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                                                                                                                                                                                                                                                                                      Staphylococcus antibacterial;
                                     Sequence 9 AA;
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                                                                                                                                                                                                                                       08-MAY-2002
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                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                               AAM50903;
                                                            Query Match
Best Local S
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AAM50903
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peptide involves: assembling a linear peptide chain on to a solid phass resin support; deprotecting the resulting protected assembled peptide; treating the deprotected peptide with neutral buffer for a time sufficient to form the cyclic peptide and cleave the peptide from the support; and recovering the cyclic peptide. The peptide is useful for bacterial interference, especially for the treatment of S. aureus
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cyclic peptide, Staphylococcus aureus, infection, antibacterial, agr response inhibitor.
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                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                      Length 9;
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1.7e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP53544 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                    94.9%; Sco
llarity 100.0%; Pr
Conservative 0;
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Matches

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This sequence represents the Staphylococcus aureus AgrDII derived peptide. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus
                                                                                                                                                                                                                                                                                                            infections with Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide-mediated quorum sensing inhibitor peptide cyclo-XII.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35; DB 3; I
Pred. No. 1.7e+06;
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                                                                                                                                                                                                                                              Novick RP,
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QUOREX PHARM INC.
UNIV TECHNOLOGIES INT INC.
                                                                                                                                                                                                                                                                                                          New cyclic peptides for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB07160 standard; peptide; 9 AA.
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                                                                                                                                 99WO-US014562.
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07-DEC-2000; 2000US-0254398P.
                                                                                                                                                                                           (UYRQ ) UNIV ROCKEFELLER.
(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                   Staphylococcus aureus.
                                                                                                                                                                                                                                             Muir TW, Mayville P,
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   virulence factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9 AA;
                                                                  WO9967286-A2
                                                                                                                              24-JUN-1999;
                                                                                                                                                              24-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BL,
                                                                                                 29-DEC-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB07160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents the Staphylococcus aureus AgrDII derived operation. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New cyclic peptides for treating infections with Staphylococcus aureus.
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                        Staphylococcus aureus infection; AgrD; agr response; treatment; virulence factor.
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Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 9;
                                                                                                                                                                                                                                        Staphylococcus aureus AgrDII derived peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus AgrDII derived peptide sequence.
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Pred. No. 1.7e+06;
l; Mismatches 1;
 Mismatches
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                                                                                                                                           AAY67860 standard, peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYNQ ) UNIV ROCKEFELLER.
(UYNY ) UNIV NEW YORK STATE
                                                                                                                                                                                                         (first entry)
9; Conservative
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                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus.
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                                                             GVNAXASLF 9
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                              GVNAXASLF
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Best Local Similarity
Matches 7; Conserv
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AAY67859

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US6337385-B1
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         Muir TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM51004;
                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                      subject.
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                                                                                       The invention relates to the use of autoinducer-2 (AI-2) agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis. Synergistic antibiotic compositions comprising inhibitors of the quorum-sensing pathway of a microorganism are also provided. Methods using such AI-2 analogues are useful for treating pathogen-associated disease states. The compounds and antibiotic compositions can be used to inhibit bacterial cell growth and/or biofilm formation on a medical device, particularly for promoting growth of skin graft replacements used in the treatment of burns and ulcers. They may also be used to aid wound repair, and to inhibit bacterial cell growth and biofilm formation in or on products or devices used for personal hygiene. The present sequence represents a inhibitor of peptide-mediated quorum sensing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "note linked to residue 9 to form cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "note linked to residue 5 to form cyclic peptide"
                            Use of autoinducer-2 agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis, also antibiotic compositions.
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic; antibacterial; infection; therapy; cyclic.
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Pred. No. 1.7e+06;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Protected peptide used in cyclic peptide production.
                                                                        Disclosure; Page 33; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "Ser(Bzl)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "Ser(Bzl)"
                                                                                                                                                                                                                                                                                                                                                                             AAM50907 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "Z-Gly"
                                                                                                                                                                                                                                                           89.78;
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NEW YORK STATE.
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                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                       1 GVNAXASLF 9
         WPI; 2002-075235/10.
                                                                                                                                                                                                                                                                                                                          1 GVNASSSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                          Sequence 9 AA;
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(UYNY ) UNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                 AAM50907;
                                                                                                                                                                                                                                                                                                                                                       RESULT 7
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The present sequence is that of a protected peptide used in an example of the preparation of novel synthetic cyclic peptides of the invention (see ANMS0899-906). The peptide corresponds to the Staphylococcus aureus areas Agroll sequence with a Cys5 to Ser mutation (lactone). It was synthesised on a Wang-resin using an Fimoo N-alpha protection strategy. Following CC chain assembly the peptide was cleaved from the support and the Ser-5 cadd:anisole:water mixture (90:5:5) for 4hr. The partially protected peptide alpha carboxylates were then dissolved in DMF and treated with PyBOP and a catalytic amount of dimethylaminopyridine. Cyclization was complete after 2 hr. The remaining protecting groups were then removed by treatment with HF and the peptide purified by HPLC. The cycliz peptide is capable of inhibiting the agr response of Staphylococcus aurens. The capable of inhibiting the agr response of Staphylococcus aurens. The crivation of this response. Replacement of the thiol ester component of the cyclic ring structure within alatone (as in the present case) or a clactam can destroy agr response activating activity while preserving and character interference, especially for the treatment of S. aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "note linked to residue 9 to form cyclic peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in
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Pred. No. 1.7e+06;
1; Mismatches 1;
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Beavis
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5
   Novick RP,
                                                                                                                                                                                                                                              Disclosure; Col 14; 18pp; English.
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Synthetic.
   Mayville P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                σ
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                                                             WPI; 2002-170774/22.
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ses 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GVNASSSLF
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Beavis R,

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AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection; therapy.
                                                           Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in
                              Muir TW, Mayville P, Novick RP,
                                                                                                                                                                                                                                                                                                                                                 AAM51003 standard; peptide; 9 AA
                                                                                         Example 1; Col 9; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                             AgrD2 linear free acid peptide.
        (UYNQ ) UNIV ROCKEFELLER. (UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYRQ ) UNIV ROCKEFELLER.
(UYNY ) UNIV NEW YORK STATE.
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Best Local Similarity 77.5-
7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muir TW, Mayville P,
                                            WPI; 2002-170774/22.
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89.7%; Scor. 77.8%; Pred 1; }

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Beavis

Novick RP,

99US-00339511 98US-0090402P

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The present sequence is that of a novel synthetic AgrD2 linear free acid peptide. The peptide is derived from the cyclic AgrD2 peptide of Staphlosocous aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virilence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a bet-lactamase reporter gene fused to the agrB3 promoter. This allowed activation or inhibition of the agr response to be monitored spectrophotometrically. Unlike an AgrD2 thiololactone crivate or inhibit the agr response, even when added to cultured cells at un concentrations. The invention provides claimed cyclic peptides (see AAM51001), the present peptide was unable to either activate or inhibit the agr response, even when added to cultured cells at un concentrations. The invention provides claimed cyclic peptides (see peptides are useful for bacterial interference, especially for the peptides are useful for bacterial interference, especially for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
                                             ø
                 Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in subject.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.7%; Score 35; DB 5; I
77.8%; Pred. No. 1.7e+06;
iive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "C-terminal thioester"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM51002 standard; peptide; 9 AA.
                                                                                                  Example 1; Col 9; 18pp; English.
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(UYNY ) UNIV NEW YORK STATE.
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Best Local Similarity 77.0
77.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-170774/22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVNAXASLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM51002;
                                                             subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM51002
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of a novel synthetic AgrD2 lactone cyclic peptide in which residue 5 of the peptide is linked to residue 9 via a lactone bond. The peptide is darived from an AgrD2 peptide of a lactone bond. The peptide is darived from an AgrD2 peptide of the control of the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The bloological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agrP3 promoter. This allowed activation or inhibition of the agr response of containing a beta-lactamase reporter gene fused to the culturating the agr response of group I S. aureus strains without activating the agr response of group I S. aureus strains. The invention provides claimed cyclic peptides (see AAMS0899-906 and AAMS0899) and convides claimed cyclic peptides (see AAMS0899-906 and AAMS0899) and can lactone bond. The cyclic peptides are useful for bacterial interference, especially for the treatment of S. aureus infection.
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Gaps

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9;

AA;

Sequence 9

 $\overset{\text{\tiny M}}{\times}\overset{\text{\tiny M}}{\overset{\tiny M}}\overset{\text{\tiny M}}{\times}\overset{\text{\tiny M}}{\times}\overset{\tiny M}}\overset{\text{\tiny M}}{\overset{\tiny M}}\overset{\text{\tiny$

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This sequence represents the Staphylococcus aureus AgrDII derived peptide. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus
activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New cyclic peptides for treating infections with Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus infection; AgrD; agr response; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.2%; Score 34; DB 3; Length 9;
88.9%; Pred. No. 1.7e+06;
ive 1; Mismatches 0; Indels
                                                                                                                                                                            0; Indels
                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus AgrDII derived peptide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beavis
                                                                                                                                   Score 34; DB 3; I
Pred. No. 1.7e+06;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ji G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novick RP,
                                                                                                                                                                                                                                                                                                                                                                           AAY67861 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Unknown
                                                                                                                                     87.2%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYRQ ) UNIV ROCKEFELLER.
(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mayville P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus
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                                                                                                                                     Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                  GVNAXSSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GVNAXASLF
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                                                                                                                                                                                                                         1 GVNAXASLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       virulence factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUN-1998;
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                                                                                               σ
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                                                                                                                                                                                                                                                                                                                                                                                                                      AAY67861;
                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                    RESULT 12
                                                                                                                                                                                                                                                                                                                                                             AAY6786:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
           888888
                                                                                                                                                                                                                            ò
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                                        The present sequence is that of a novel synthetic AgrD2 linear thioester peptide. The peptide is derived from the cyclic AgrD2 linear thioester peptide. The peptide is derived from the cyclic AgrD2 peptide of Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. augreus strains containing a beta-lactamase reporter gene fused to the agrp3 promoter. This allowed activation or inhibition of the agr response to be monitored spectrophotometrically. Unlike an AgrD2 thiololactone crivate or inhibit the agr response, even when added to cultured cells at um concentrations. The invention provides claimed cyclic peptides are useful for bacterial interference, especially for the peptides are useful for bacterial interference, especially for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a cyclic peptide derived from the Staphylococcus aureus AgrD peptide. The invention relates to AgrD derived peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New cyclic peptides for treating infections with Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus infection; cyclic peptide; AgrD; agr response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                          89.7%; Score 35; DB 5; Length 9; 77.8%; Pred. No. 1.7e+06; ive 1; Mismatches 1; Indels

    S. aureus peptide #1 used for bacterial interference.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ji G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novick RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY67851 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; Page 26; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Unknown
               Example 1; Col 9; 18pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US014562
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(UXNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   virulence factor; treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mayville P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GVNAASSLF. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GVNAXASLF 9
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25-APR-2000

AAY67851;

RESULT 11

ò a Misc-difference

WO9967286-A2

24-JUN-1998;

Muir TW,

24-JUN-1999;

29-DEC-1999

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Gaps

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13-MAR-2002

ABB07161;

Synthetic.

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The present sequence is that of a novel synthetic AgrD2 lactam cyclic peptide in which residue 5 of the peptide is linked to residue 9 via a lactar bond. The peptide is derived from an AgrD2 peptide 0 via a staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide. Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide. Where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agr spectrophotometrically. The AgrD3 lactam peptide to be monitored spectrophotometrically. The AgrD3 lactam peptide in protein agr response in group I S. aureus strains and did not activate the agr response in group I S. aureus strains and did not cortivate the agr response in group I N in or III strains. The invention provides claimed cyclic peptides (see AAWS0899-906 and AAMS0899) and methods for preparing them, especially where the cyclic bond is a lactam or lateratence, especially for the treatment of S. aureus infection.
                                                                                                                                                                                                                                                                                                                                                                                  /note= "note linked to residue 5 to form cyclic peptide"
                                                                                                                                                                                                                                                                                                  "note linked to residue 9 to form cyclic peptide"
                                                                                                                         AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.2%; Score 34; DB 5; Length 9;
88.9%; Pred. No. 1.7e+06;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beavis R,
                                                                                                                                                                                                                                                                                                                                              'note= "any amino acid"
                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novick RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAMS0908
ID AAMS0908 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-00339511.
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                                                                                AgrD2 lactam cyclic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYRQ ) UNIV ROCKEFELLER.
(UYNY ) UNIV NEW YORK STATE.
                    (revised)
(first entry)
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Best Local Similarity 88.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muir TW, Mayville P,
                                                                                                                                                                                         Staphylococcus aureus..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-170774/22.
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                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                  therapy; cyclic
                                                                                                                                                                                                                                                                                                                                                                Misc-difference
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                    07-AUG-2003
08-MAY-2002
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                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subject,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to the use of autoinducer-2 (AI-2) agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis. Syneaystate antibiotic compositions comprising inhibitors of the quorum-sensing pathway of a microorganism are also provided. Methods using such AI-2 analogues are useful for treating pathogen-associated disease states. The compounds and antibiotic compositions can be used to inhibit bacterial cell growth and/or biofilm formation on a medical device, particularly for promoting growth of skin graft replacements used in the treatment of burns and ulcers. They may also be used to aid wound repair, and to inhibit bacterial cell growth and biofilm formation in or on products or devices used for personal hygiene. The present sequence represents a inhibitor of peptide-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoinducer-2 agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis, also antibiotic compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Surette MG;
                                                                                                                                                                                                                                Autoinducer-2; AI-2; antibiotic; antibacterial; dermatological; vulnerary; pheromone; agr system; accessory gene regulator; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                         Peptide-mediated quorum sensing inhibitor peptide cyclo-XIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stein J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34; DB 5; Length 9;
Pred. No. 1.7e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                    'note= "diaminoprprionic acid residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shokat K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schauder S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 33; 134pp; English.
                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYPR-) UNIV PRINCETON.
(QUOR-) QUOREX PHARM INC.
(UYTE-) UNIV TECHNOLOGIES INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM51005 standard; peptide; 9 AA.
                                                           ABB07161 standard; peptide; 9 AA
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                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dammel
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVNAXSSLF
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                                                                                                                                                                                                                                                                                                                                           Key
Modified-site
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BL,

Bassler

15-NOV-2001

Ji G;

·.

Gaps

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AAM51005;

RESULT 14 AAM51005

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/note= "note linked to residue 5 to form cyclic peptide"
                                                                                                                                                                                                                                                                                                    Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in a subject.
                                                Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic; antibacterial; infection; therapy; cyclic.
                                  Protected peptide used in cyclic peptide production.
                                                                                                                                                                                                                                                                         Muir TW, Mayville P, Novick RP, Beavis R,
                                                                                    Location/Qualifiers
                                                                                                   'note= "Z-Gly"
                                                                                                                                                                                                                       99US-00339511.
                                                                                                                                                                                                                                    98US-0090402P.
                                                                                                                                                                                                                                                  (UYNQ ) UNIV ROCKEFELLER.
(UYNY ) UNIV NEW YORK STATE.
                     (first entry)
                                                                                                                                                                                                                                                                                       WPI; 2002-170774/22.
                                                                                                                                                                    Misc-difference
                                                                                                          Misc-difference
                                                                                      Key
Modified-site
                                                                                                                        Modified-site
                                                                                                                                       Modified-site
                                                                                                                                                     Modified-site
                                                                                                                                                                                                                      24-JUN-1999;
                                                                                                                                                                                                                                     24-JUN-1998;
                     08-MAY-2002
                                                                                                                                                                                          US6337385-B1
                                                                                                                                                                                                        08-JAN-2002
                                                                       Synthetic
      AAM50908
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note= "Ser(Bzl)" note= "Ser(Bzl)" 'label = Dpr(Boc)

Ji G;

note= "note linked to residue 9 to form cyclic peptide"

The present sequence is that of a protected peptide used in an example of the preparation of novel synthetic cyclic peptides of the invention (see AAMS0899-06). The peptide corresponds to the Staphylococcus aureus AAMS089-060. The peptide corresponds to the Staphylococcus aureus april sequence with a Cys5 to diaminopropionic acid (Dpr) mutation (lactam). It was synthesised on a Wang-resin using an Fmoc N-alpha protection strategy. Following chain assembly, the peptide was cleaved from the support and the Dpr-5 residue deprotected by treatment with a trifluoroacetic acid-anisole:water mixture (90:5:5) for 4 hr. The partially protecting groups were removed by treatment with HF and the peptide purified by HPLC. The cyclic peptide is capable of inhibiting the remaining protecting groups were removed by treatment with HF and the peptide purified by HPLC. The cyclic peptide is capable of inhibiting the active AgrD peptides is required for activation of this response. Replacement of the thiol ester component of the cyclic ring structure within a lactam (as in the present case) or a lactone can destroy agr activity. The cyclic peptides are useful for bacterial interference, especially for the treatment of S. aureus infection Disclosure; Col 14; 18pp; English.

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Query Match 87.2%; Score 34; DB 5; Length 9; Best Local Similarity 88.9%; Pred. No. 1.7e+06; Matches 8; Conservative 1; Mismatches 0; Indels
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Sequence 9 AA;

Gaps

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6 GVNAXASLF ઠે g

Search completed: October 26, 2004, 15:59:44 Job time : 44.75 secs

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October 26, 2004, 15:54:00; Search time 31.5 Seconds (without alignments) 92.502 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUBL pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUBL pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUBL pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO9B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9B_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO08_NEW PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO08_NEW PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USIOB_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/2/pubpaa/USIOD_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USIOD_PUBCOMB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/USIO_NEW PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1364641 seqs, 323758627 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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39
1 GVNAXASLF 9
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                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

g.	e 5, Appli	e 1, Appli	m	9	722	e 40441, A	e 2, Appli		e 11888, A	٠.	e 2, Appli	e 7334, Ap	
Description	Seguence 5, 7	Sequence	Sequence	Sequence	Seguence	Seguence	Seguence	Seguence	Seguence	Seguence	Seguence	Seguence	Seguence
ΩI	US-10-032-950-5	US-10-032-950-1	US-10-201-444-3	US-10-201-444-6	US-10-282-122A-72245	US-10-767-701-40441	US-10-243-351-2	US-10-032-950-6	US-10-369-493-11888	US-10-369-493-14064	US-10-032-950-2	US-09-864-408A-7334	US-10-282-122A-53320
	13	13	14	14	15	16	14	13	14	14	13	11	15
% Query Match Length DB	9	o	σ	47	271	294	490	6	279	800	6	147	340
% Query Match	94.9	87.2	84.6	84.6	82.1	82.1	82.1	79.5	79.5	79.5	76.9	76.9	76.9
Score	37	34	33	33	32	32	32	31	31	31	30	30	30
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equence 526 equence 631 equence 163 equence 229 equence 18	equence 12 equence 11 equence 7, equence 19 equence 19	2 4 1 1 2 2 4 2 6 1 2 9 4		equence 45 equence 45 equence 45 equence 45 Sequence 4 Sequence 4 Sequence 4
5 US-10-282-122A-5267 5 US-10-282-122A-6311 4 US-10-292-798-1638 4 US-10-017-161-2252 4 US-10-292-798-1998 5 US-10-282-122A-7802	6 US-10-437-963-12075 6 US-10-437-963-111281 1 US-10-437-963-19782 6 US-10-437-963-19782 6 US-10-767-701-40852	5 US-10-282-122A-480 4 US-10-145-586-46 0 US-10-369-493-1219 0 US-09-826-509-561 4 US-10-225-567A-296	5 US-10-425-114-5 US-00-424-139-1	US-09-938-418-9 US-09-938-418-9 US-09-99-8192A-45 US-09-99-8132A-45 US-09-978-183A-45 US-09-978-688A-4 0 US-09-978-688A-4 0 US-09-978-688A-4 0 US-09-978-688A-4
347 1 396 1 415 1 432 1 572 1				7.4477744477744477744777447774777477747
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ALIGNMENTS

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RESULT 1
US-10-132-950-5
Sequence 5, Application US/10032950
Sequence 5, Application US/10032950
Sequence 5, Application No. US20020077453A1
GENERAL INFORMATION:
APPLICANT: Mary 10, Patricia
APPLICANT: Mary 110, Patricia
APPLICANT: Beavis, Ronald
APPLICANT: Beavis, Ronald
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/10/032,950
CURRENT FILING DATE: 2001-12-27
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 5
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: peptide; NAME/KEY: VARIANT; LOCATION: (5); OTHER INFORMATION: Xaa represents any amino acid at this position. US-10-032-950-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
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Query Match
94.9%; Score 37; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 1 GVNAXASLF

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APPLICANT New YOLK University Medical Center
TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
FILE REFERENCE: 67753/7
CURRENT APPLICATION NUMBER: US/10/201,444
CURRENT FILING DATE: 2002-07-23
PRIOR FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 9
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                                                                                                                                     Sequence 1, Application US/10032950

Publication No. US2002007745341

GENERAL INFORMATION:

APPLICANT: Mayville, Patricia

APPLICANT: Mo. US20020077453A1ick, Richard P.

APPLICANT: No. US20020077453A1ick, Richard P.

TITLE OF INVENTION: NONEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL

TITLE OF INVENTION: INTERFERENCE

FILE REFERENCE: 600-1-21N

CURRENT FILING DATE: 2001-12-27

PRIOR PELING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: Description of Artificial Sequence: Synthetic COTHER INFORMATION: peptide NAME/REY: VARIANT LOCATION: (5) LOCATION: (5) CTHER INFORMATION: Xaa represents any amino acid at this position. US-10-032-950-1
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84.6%; Score 33; DB 14; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.2e+06;
Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.2%; Score 34; DB 13; Length 9; 88.9%; Pred. No. 1.2e+06; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 3, Application US/10201444; Publication No. US20030078378A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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GVNAXSSLF 9
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GVNAXASLF
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Sequence 6, Application US/10201444

Publication No. US20030078378A1

SERERAL INFORMATION:

APPLICANT: New York University Medical Center

TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS

FILE REFERENCE: 637-37

CURRENT APPLICATION NUMBER: US/10/201,444

CURRENT FILING DATE: 2002-07-23

PRIOR PRILING DATE: 1997-05-22

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin version 3.0

FROM DATE: ALTERNATE: PATENTIN VERSION 3.0

SEQ ID NO 6
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPRENCE: ELITRA-034A
CURRENT APPLICATION NUMBER: 105/10/282,122A
CURRENT RILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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NUMBER OF SEQ ID NOS: 78614
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Pred. No. 3.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 72245, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,646
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,646
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PELING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-01-03
PRIOR PELICATION NUMBER: 60/24,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-201-444-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.8%;
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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SOFTWARE: PatentIn version 3.1

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VS-10-369-493-11888

i) Sequence 11888, Application US/10369493

j) Sequence 11888, Application No. US20030233675A1

j) GENERAL INFORMATION:
    APPLICANT: CAP. Yongweit

j) APPLICANT: Slater, Steven C.
    APPLICANT: Glodman, Barry S.
    APPLICANT: Chen, Alanfeng
    TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN FLANTS FOR PRODUCTION OF
    TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN FLANTS FOR PRODUCTION OF
    TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
    PRIOR FILING DATE: 2003-02-28
    PRIOR FILING DATE: 2003-02-21
    NUMBER OF SEQ ID NOS: 47374
    LENGTH: 279
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0
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                                                                           Gaps
                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/10032950; Publication No. US20020077453A1
GENERAL INFORMATION:
APPLICANT: Muir, Ton
APPLICANT: Mayville, Patricia
APPLICANT: Mo. US20020077453A1ick, Richard P.
APPLICANT: Deavis, Ronald
APPLICANT: Deavis, Ronald
APPLICANT: Deavis, Ronald
APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
ITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-21
FILE REPERENCE: 600-1-21
CURRENT APPLICATION NUMBER: US/10/032,950
CURRENT APPLICATION NUMBER: 60/090,402
FRIOR PALING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
NAME/KEY: VARIANT
LOCATION: (5)
OTHER INFORMATION: Xaa represents any amino acid at this position. US-10-032-950-6
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0
           Score 32; DB 14; Length 490;
Pred. No. 79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 31; DB 13;
Pred. No. 1.2e+06;
                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                    82.1%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
                 Query Match
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 79.5
Best Local Similarity 77.6
Matches 7; Conservative
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US-10-032-950-6
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APPLICANT: Castleberry, Tessa A.
APPLICANT: Lu, shions
APPLICANT: Lu, shions
APPLICANT: Cwen, Thomas A.
APPLICANT: Smock, Steven
TITLE OF INVENTION: DNA ENCODING THE CHIMPANZEE PROSTAGLANDIN E2 RECEPTOR EP4 SUBTYPE
FILE REPERENCE: PC11827AGFP
CURRENT APPLICATION NUMBER: US/10/243,351
CURRENT PILING DATE: 2002-09-13
PRIOR FILING DATE: 2001-09-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 40441, Application US/10767701

Publication No. US20040172684A1

Publication No. US20040172684A1

Publication No. US20040172684A1

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cac, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

TITLE OF INVENTION: 18-2153353 B

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 40441

LENGTH: 294
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                                                                                                                                                             DB 15; Length 271;
                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , OTHER INFORMATION: Clone ID: SORBI-28MAY03-C60451_1.pep
US-10-767-701-40441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure
LOCATION: (1)..(294)
PHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                             Query Match
Best Local Similarity 77.8%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10243351 Publication No. US20030059890A1 GENERAL INFORMATION:
                       LENGTH: 271
TYPE: PRT
ORGANISM: Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                             120 GVNPYASLF 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:|: ||||
255 GLNSTASLF 263
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; ORGANISM: chimpanzee
US-10-243-351-2
                                                                                                        US-10-282-122A-72245
                                                                                                                                                                                                                                                                                                                                                                                                                                        -10-767-701-40441
SEQ ID NO 72245
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LENGTH: 490
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76.9%; Score 30; DB 13; Length 9; larity 77.8%; Pred. No. 1.2e+06; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haeelbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
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Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
                                                                                                     1 GVNAXASLF 9
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  Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                 1 GANAXSSLF
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US-10-366-493-14064

Sequence 14064, Application US/10369493

Publicated No. US2030233675A1

Sequence 14064, Application US/10369493

Publication No. US2030233675A1

APPLICANT: Cao, Yongwei

APPLICANT: Galdman, Barry Gregory J.

APPLICANT: Glodman, Barry S.

APPLICANT: Goldman, Barry S.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: USAPESSION OF MICROBIAL PROPERTIES

FILE REFERENCE: 38-10 (52052) B

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-28

PRIOR FILING DATE: 2002-02-28

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 14064

LENGTH: 800

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; Publication W. US20020077453A1
; Publication W. US20020077453A1
; GENERAL INFORMATION:
APPLICANT: Mayville, Patricia
APPLICANT: Mayville, Patricia
APPLICANT: Mayville, Ronald
APPLICANT: UJ, GUANGYONG
TITLE OF INVENTION: INTERFERENCE
TITLE OF INVENTION: INTERFERENCE
TITLE OF INVENTION: NUMBER: US/10/032,950
TITLE OF INVENTION NUMBER: US/10/032,950
FRICK APPLICATION NUMBER: 60/090,402
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR APPLICATION NUMBER: 60/090,402
SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 8
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; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-2
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  Query Match 79.5%; Score 31; DB 14; Length 279; Best Local Similarity 87.5%; Pred. No. 73; Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.5%; Score 31; DB 14; Length 80 ilarity 77.8%; Pred. No. 2.3e+02; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Pseudomonas fluorescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT VORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 GVTALASLF 141
                                                                                                                                               139 GVNAFASĽ 146
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Best Local Similarity
Matches 7; Conserva
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Sequence 7334, 2020(40009474A)
Sequence 7334, 2020(40009474A)
Sequence 7334, 2020(40009474A)
GENERL INFORMATION:
Bublication No. US20040009474A1
GENERL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: NO. US20040009474A1e1 Human Polynuclectides and Polypeptides Encorpance 2140-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 9068
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 147
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APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yau, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: 60/120,0
PRIOR APPLICATION NUMBER: 60/120,0
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1) ...(1)
CTHER INFORMATION: Wherein Xaa may be any naturally occuring amino acid
US-09-864-408A-7334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Gaps

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APPLICANT: Xu, H,

APPLICANT: Xu, H,

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: 60/200, 848
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-06-23
PRIOR PILING DATE: 2000-06-23
PRIOR PLING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: 60/200, 335
PRIOR FILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-22
PRIOR PLING DATE: 2000-10-20-16
PRIOR PLING DATE: 2000-10-20-16
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                                                                                                                                                                                                              Score 30; DB 15; Length 347;
Pred. No. 1.6e+02;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 63115, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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US-10-282-122A-63115
                                                                                              ; TYPE: PRT
; ORGANISM: Clostridium botulinum
US-10-282-122A-52679
SOFTWARE: PatentIn version 3.1
SEQ ID NO 52679
LENGTH: 347
                                                                                                                                                                                                                     Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
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Wall, Daniel
Trawick, John
Carr, Gran
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 66.7
Matches 6; Conservative
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APPLICANT: Xu, H.
APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2000-03-21
PRIOR PPLICATION NUMBER: 60/206,848
PRIOR PPLICATION NUMBER: 60/206,848
PRIOR PPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-10-20
PRIOR PLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-11-27
PRIOR PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2001-02-09
PRIOR PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-16
                              PRIOR FILING DATE: 2000-09-09
PRIOR PLILNG DATE: 2000-10-29
PRIOR PLILNG DATE: 2000-10-23
PRIOR PLILNG DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PELICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR PAPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR RILING DATE: 2001-02-09
PRIOR RILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
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Pred. No. 1.5e+02;
3; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Clostridium difficile
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin version 3.1
SEQ ID NO 53320
LENGTH: 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamco, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match. 76.9
Best Local Similarity 55.6
Matches 5; Conservative
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98 GINSGAALF 106
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Search completed: October 26, 2004, 16:10:12 Job time : 31.5 secs

us-10-032-950-5.rapb

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

October 26, 2004, 15:46:55 ; Search time 8.73529 Seconds (without alignments) 99.132 Million cell updates/sec Run on:

US-10-032-950-5 39 1 GVNAXASLF 9

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
'1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		· d			SOMMAKIES	
Result		Query			;	
. i	Score	Match	Length	8 : B	GI .	Description
H	37	94.9	333	Н	C69812	ferrichrome ABC tr
7	33	84.6	47	~	C89995	AgrD protein [impo
ო	32	82.1	382	~	A28067	lysosomal membrane
4	32	82.1	405	~	A60534	P2B/LAMP-1 precurs
ហ	32	ä	407	8	A30200	120K lysos
9	31	6	349	~	S74439	iron(III) dicitrat
7	31	6	468	~	T24523	hypothetical prote
σ0	30	9		~	B38116	
თ	30	76.9		7	AC2563	transposase alr850
10	30	9		N	S60885	in
11	30	9		N	AG2524	transposase all737
12	30	θ.		7	A12490	se
13	30	è.		N	AG2491	se a
14	30	Ġ		~	AD2478	transposase all700
15	30	ė		N	A12499	Φ
16	30	ġ.		N	AF2515	Φ
	30	ģ		N	T11068	cytochrome-c oxida
18	30	76.9		N	AB2129	iron(III) dicitrat
19	30	ů.		N	AD3198	ical
20	30	è.		N	A83391	glut
21	30	Ġ.		~	B83609	gJn
22	30	ģ		N	AC2518	se
23	30	76.9		N	AC2564	transposase alr851
24	30	ġ		(7)	AD2511	
25	30	9		N	AC0325	urease (EC 3.5.1.5
26	30	è.	ιΩ	N	836028	BC 3.
27	30	76.9		C)	F83779) di
28	30	9	12	N	0616	gree
29	29	74.4	109	N	N	hypothetical prote

probable membrane	prostaglandin E2 r	zip protein precur	hypothetical prote	probable flagellar	protein Y32F6A.3 [RNA binding protei	receptor-protein k	C2H2 type zinc fin	hypothetical prote	flagellar biosynth	flagellar biosynth	polyamine transpor	iron(III) dicitrat	fructose-bisphosph	protein M homolog
D97308	A53572	EPFF	T33320	H71562	G89189	T41065	T45786	T40120	D83354	AD1159	AD1518	E83194	D69805	A44942	B43715
N	0	н	7	~	~	~	N	0	(1	7	~	~	0	~	Ŋ
148	488	200	570	605	655	703	895	1238	186	255	255	297	333	369	369
74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	71.8	71.8	71.8	71.8	71.8	71.8	71.8
53	29	29	29	29	59	59	29	53	28	58	28	28	28	28	28

ALIGNMENTS

RESULT 1

 C69812
ferrichrome ABC transporter (permease) homolog yfmD - Bacillus subtilis
 C;Species: Bacillus subtilis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C,Accession: C69812
R; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A, Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: C69812
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-333 <KUN>
A;Cross-references: UNIPROT:034933; GB:Z99108; GB:AL009126; NID:g2633055; PIDN:CAB12580
C;Genetics:
A;Experimental source: strain 168
C;Genetics:
A;Genetics:
A;Geneti

.. Query Match Best Local Similarity 88.9%; Pred. No. 0.53; Matches 8; Conservative 0; Mismatches 1; Indels

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Gaps

99 GVNAGASLF 107 1 GVNAXASLF 9 ò g

RESULT 2 C89995

AgrD protein [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: OrMay-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: C89995
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.

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NyAlternate names: protein slr1317

NyAlternate names: protein slr1317

Cispecies: Synechocystis sp.

Cispecies: Synechocystis
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A; Residues: 1-407 < HOW.
A; Cross-references: UNIPROT: F14562; EMBL: J03672
A; Oross-references: UNIPROT: F14562; EMBL: J03672
A; Note: the authors translated the codon GGG for residue 15 as Val
R: Himeno, M:; Noguchi, Y.; Sasaki, H.; Tanaka, Y.; Furuno, K.; Kono, A.; Sakaki, Y.; Kat
ERBS Lett. 244, 351-356, 1989
A; Title: Isolation and sequencing of a cDNA clone encoding 107 kDa sialoglycoprotein in
A; Reference number: S03331; MUID: 89153580; PMID: 2920835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 22-407 <HIM>
A; Cross-references: EMBL: X14765; NID: 956577; PIDN: CAA32873.1; PID: 956578
A; Note: part of this sequence, including the amino end of the mature protein, C; Superfamily: lysosome-associated membrane protein
C; Superfamily: lysosome-associated membrane protein
C; Reywords: 91ycoprotein; membrane protein
F; 22-407/Product: lysosomal membrane glycoprotein, 107K #status experimental <MAT>
                                                                                                                     A,Molecule type: DNA
A,Residues: 1-34 sKAN-
A,Cross-references: UNIPROT: P72591; EMBL:D90899; GB:AB001339; NID:g1651650; PIDN:BAA1659
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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A;Accession: S74439
A;Status: nucleic acid sequence not shown; translation not shown
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Pred. No. 11;
2; Mismatches 1; Indels
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A,Accession: A30200
                                                                                - rat
                                                                         lysosomal membrane glycoprotein precursor
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Best Local Similarity 66.7%;
Matches 6; Conservative
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P2B/LAMP-1 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Nar susculus (house mouse)
C;Accession: A60534
R;Heffernam, M: Yousefi; S:; Dennis, J.W.
Cancer Res 49, 6077-6084, 1989
A;Title: Molecular characterization of P2B/LAMP-1, a major protein target of a metastasi
A;Reference number: A60534; MUID:90002989; PMID:2676155
A;Accession: A60534
A;Accession: A6053
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() Species: Mus musculus (house mouse)
() Species: Musculus (house)
() Species: Musculus (house)
() Species: Musculus (house)
() Species: Musculus (house)
() Muscu
A,Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: C89995
A;Catucus: preliminary
A;Molecule type: DNA
A;Residues: 1-47 <KUR>
A;Cross-references: UNIPROT:033586; GB:BA000018; PID:g13701831; PIDN:BAB43124.1; GSPDB:G
A;Experimental source: strain N315
C;Genetics:
A;Gene: agrD
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GMNASSSLF 287
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                                                  Length 349;
                                                                            Indels
                                                  Score 31; DB 2;
Pred. No. 16;
0; Mismatches
A,Gene: fecD
C,Superfamily: vitamin B12 transport protein btuC
C,Keywords: iron transport
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RESULT 7

RESULT 5

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transposase all7375 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Accession: 44-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AG2524
B;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An A;Reference number: AB1807; MUD:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mycobacterium smegmatis
C;Species: Mycobacterium smegmatis
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
R;Fiss, E.H.; Yu, S; Jacobs Jr., W.R.
Mol. Microbiol. 14, 557-569, 1994
A;Title: Identification of genes involved in the sequestration of iron in mycobacteria: A;Title: Identification of genes involved in the sequestration of iron in mycobacteria: A;Molecule type: DNA
A;Residues: 1-234 *RIS>
A;Molecule type: DNA
A;Residues: 1-234 *RIS>
A;Residues: 1-234 *RIS>
A;Gross-references: UNIPROT:Q50375; EMBL:U10425; NID:g595400; PIDN:AAC43258.1; PID:g595-A;Genetics: A;Gene: fxuC
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A;Molecule type: DNA
A;Residues: 1-247 <KURN>
A;Cross_references: UNIPROT:Q8YKC5; GB:BA000020; PIDN:BAB77133.1; PID:g17134574; GSPDB:
A;Experimental source: strain PCC 7120
C;Genetics:
A;Cross-references: UNIPROT:QBYK27; GB:AP003604; PIDN:BAB77421.1; PID:gl7134865; GSPDB:CA;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: plasmid
C;Superfamily: Anabaena insertion sequence IS892 hypothetical protein 2
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C;Superfamily: Anabaena insertion sequence IS892 hypothetical protein
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Pred. No. 19;
2; Mismatches 1; Indels
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Pred. No. 18;
3; Mismatches
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55.6%;
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
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64 GLSATASLF 72
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37 GINSGAALF 45
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| GLSATASLF 13
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les 6; Conserv
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A,Note: Nostoc sp. PCC 7120  
A,Note: Nostoc sp. strain PCC 7120  
E, Note: Note:
                                            hypothetical protein T05E11.5 - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C,Accession: T24523
R,Kershaw, J.
submitted to the EMBL Data Library, January 1996
A,Refeatus: preliminary; translated from GB/EMBL/DDBJ
A,Rocession: T24523
A,Rolecule type: DNA
A,Residues: 1-468 <WIL>
A,Residues: 1-468 <WIL>
A,Cross-references: UNIPROT: P49049; EMBL: Z68751; FIDN: CAA92975.1; GSPDB: GN00022; CESP:T0
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A;Title: Characterization of insertion sequence IS892 and related elements from the cyan A;Reference number: A38116; MUD:91358369; PMID:1653218

A;Accession: B38116

A;Status: preliminary

A;Molecule type: DNA
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C;Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 09-Jul-2004
C;Accession: B38116
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C.Genetics:
A.Mobile element: insertion sequence IS892
C.Superfamily: Anabaena insertion sequence IS892 hypothetical protein 2
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Pred. No. 14;
2; Mismatches
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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5 GLSATASLF 13
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A;Molecule type: DNA
A;Residues: 1-188 <KUR>
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A;Map position: 4
A;Introns: 23/3; 293/3
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Best Local Similarity 66.7
Matches 6; Conservative
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les 6; Conserv
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A; Residues: 1-247 < KUR>
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64 GLSATASLF
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A;Residues: 1-247 <KUR>
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Best Local S
Matches 6
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Arabosase all7105 [imported] - Nostoc sp. (strain PCC 7120) plasmid pcC7120alpha (Species: Nostoc sp. PCC 7120 (Sp. Strain PCC 7120) (Sp. Sp. Strain PCC 7120) (Sp. Strain PCC 7120)
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. B, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
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AD2478
Ltransposase all7004 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AD2478
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
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A;Experimental source: strain PCC 7120
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C;Superfamily: Anabaena insertion sequence IS892 hypothetical protein
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Pred. No. 19;
2; Mismatches 1; Indels
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Pred, No. 19;
2; Mismatches 1; Indels
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Best Local Similarity 66.7%;
Matches 6; Conservative
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GLSATASLF 72
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GLSATASLF 72
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A,Molecule type: DNA
A,Residues: 1-247 <KUR>
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Nakasadi, N.; Shimpo, S.; Sugimoto, N.; Takazawa, M.; Yamada, M.; Tabata, S. DNA, Res. 6, 205-211, 200 States of the Filamentous Nitrogen-fixing Cyanobacterium Analy Reference number: Ballon; Mulli-159505; PMID:11759440

A.Reference number: Ballon; Mulli-2159526; PMID:11759440

A.Reference number: Ballon; PRID:11704

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GenCore version 5.1.6
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OM protein - protein search, using sw model

October 26, 2004, 15:44:50; Search time 40.6324 Seconds (without alignments) 127.445 Million cell updates/sec Run on:

US-10-032-950-5 39 1 GVNAXASLF 9 Title: Perfect score: Sequence:

Scoring table:

1825181 seqs, 575374646 residues BLCSUM62 Gapop 10.0 , Gapext 0.5 Searched: 1825181

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	034933			8		8	Cae92751 staphyloc		Cae92757 staphyloc	Q89ev1 bradyrhizob	Q8xhh9 clostridium			Q6zm65 brachydanio	φ	Q8dvx3 streptococc	E	Q8vh34 mus musculu	P14562 rattus norv	Q9dc13 mus musculu	Q95kz0 pan troglod	Q9m838 arabidopsis		Cad61194 dirofilar	Q98k81 rhizobium 1			Q9pky0 chlamydia m		Q6fwd3 candida gla	xanthomo
SUMMARIES		QI	034933	033586 .	Q7A2N4	Q7A4I7	CAE92745	CAE92748		LO.	CAE92757	Q89EV1	бекни б	Q922T9	Q8HN50	Q6ZM65		OXA1 STRMU	LMP1_MOUSE	Q8VH34	LMP1_RAT		PE24_PANTR	Q9M838	Q70US2	CAD61194	Q98K81	P72591	YJ95 CAEEL	Q9PK <u>Y</u> 0	Q876F4	QEFWD3	Q70C52
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Cae52334 xanthomon	Q9rck4 streptococc	Q8yk27 anabaena sp	Q50375 mycobacteri	Q94uz5 leishmania	Q8xgal anabaena sp	Q8ykc5 anabaena sp	Q78br1 carassius a	Q98se3 carassius a	047576 onchocerca	Q737n6 bacillus ce	Aas41526 bacillus	Q6hic7 bacillus th	Q8xm78 clostridium
CAE52334	Q9RCK4	Q8YK27	Q50375	Q94UZ5	Q8XGA1	Q8YKC5	Q78BR1	Q98SE3	047576	Q737N6	AAS41526	Q6HIC7	Q8XM78
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79.5	76.9	6.92	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9	76.9
31	30	30	30	30	30	30	30	30	30	30	30	30	30
32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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SEQUENCE
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of the Bacillus subtilis genome reveal genes for a new two-component system, three spore germination proteins, an iron uptake system and a general stress response protein.";
General 184:191-199(1997).
EXEL; 299108; CAB12580.1; -.
EXEL; 299108; CAB12580.1; -.
PIR; C69812; C69812.
HSSP; po6609; ILTV.
GO; GO:0005215; Fitransporter activity; IEA.
GO; GO:0005215; Fitransport, IEA.
InterPro; IRR00522; FeCD.
Fram; PF01032; FeCCD; 1.
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A GOGETKE C., Dasbach S., Kuemmel M., Wolz C.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AFF001782; GERS2745.1; -..
EMBL, AJ517715; CAE92745.1; -..
EMBL, AJ517716; CAE92745.1; -..
EMBL, AJ517716; CAE92745.1; -..
EMBL, AJ517716; CAE92757.1; -..
EMBL, AJ517719; CAE92757.1; -...
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JG., Beavis R., Novick R.P.;
"Bacterial interference caused by autoinducing peptide variants.";
Science 276:2027-2030(1997).
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Pred. No. 3.6;
0; Mismatches 1; Indels
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Pred. No. 4.2;
1; Mismatches 1; Indels
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SEQUENCE 333 AA; 35098 MW; 9F4BE91BB0EE6761 CRC64;
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Last sequence update)
Last annotation update)
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Bacteria, Firmicutes; Bacillales, Staphylococcus.
NCBI_TaxID=1280;
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Best Local Similarity 88.3...
8; Conservative
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BEDLINES-1311952; PubMed=11418146;

Kuroda M., Ohte T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Kuroda M., Ohte T., Uchiyama I., Baba T., Lian J.-Q., Ito T.,

Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

Mizuteni-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,

Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,

Mihole genome sequencing of meticillin-resistant Staphylococcus
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Pred. No. 4.2;
1; Mismatches 1; Indels
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                 Staphylococcus aureus (strain Mu50 / ATCC 700699)
Bacteria, Firmicutes, Bacillales, Staphylococcus.
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                                                                                             AgrD protein.
Name=agrD; OrderedLocusNames=SAV2037;
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EMBL, AP003135; BAB43124.1;
InterPro, IPR009229; AgrD.
Pfam; PF05331, AgrD, 1.
Complete proteome.
SEQUENCE 47 AA; 5140 MM:
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EMBL, AP003364; BAB58199.1; -
InterPro; IPR009229; AgrD.
Pfam; PF05931; AgrD; 1.
Complete proteome.
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 77.8
For 7, Conservative
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47 AA.

PRELIMINARY;

Q7A2N4 Q7A2N4;

RESULT 3
Q7A2N4
ID Q7A2N

Gaps

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CAE92745

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SEQUENCE FROM N.A.
STRAIN=gt16a-cp8;
STRAIN=gt16a-cp8;
STRAIN=gt16a-cp8;
STRAIN=gt16a-cp8;
Strains Stable S., Kuemmel M., Wolz C.;
"Evolutionary Models for the Development of the Polymorphic Loci agr and cap in Staphylococcus aureus.";
Submitted (DEC-2023) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ617717; CAE927511; -.
SEQUENCE 47 AA; 5149 MW; 22893764DFS4BFA7 CRC64;
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Goerke C., Dasbach S., Kuemmel M., Wolz C.;
Goorld C., Dasbach S., Kuemmel M., Wolz C.;
"Foolutionary Models for the Bevelopment of the Polymorphic Loci agr and cap in Staphylococcus aureus."
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ617718; CAE92754.1;
SEQUENCE 47 AA; 5149 WW; 22893764DF54BFA7 CRC64;
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STRAIN-gt111-cp8;
Goerke C., Dasbach S., Kuemmel M., Wolz C.;
"Evolutionary Models for the Development of the Polymorphic Loci agrand cap in Staphylococcus aureus.";
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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Last annotation update)
                         Staphylococcus aureus.
Bacteria, Firmicutes, Bacillales, Staphylococcus.
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Bacteria, Firmicutes, Bacillales, Staphylococcus.
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Pred. No. 4.2;
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Pred. No. 4.2;
1; Mismatches
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Best Local Similarity 77.0
Best Local 7, Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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24 GVNACSSLF
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SEQUENCE FROM N.A.
                                                                                         NCBI_TaxID=1280;
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AGRD.
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CAE92757;
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CAE92754;
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CN NCBI
RN ILL
RP SECU
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Goorke C., Dasbach S., Kuemmel M., Wolz C.;
Goorke C., Dasbach S., Kuemmel M., Wolz C.;
architionary Models for the Development of the Polymorphic Loci agr and cap in Staphylococcus aureus.";
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ617715; CAB92745.1;
SEQUENCE 47 As, 5149 MN; 22893764DF54BFA7 CRC64;
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Goerke C., Dasbach S., Kuemmel M., Wolz C.;
Goerke C., Dasbach S., Kuemmel M., Wolz C.;
"Evolutionary Models for the Development of the Polymorphic Loci agr and cap in Staphylococcus aureus.";
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ617716; CAE92748.1;
SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;
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                                                                                                                                                                                   CAE92745;
01-APR-2004 (TrEMBLrel. 27, Created)
01-APR-2004 (TrEMBLrel. 27, Last sequence update)
01-APR-2004 (TrEMBLrel. 27, Last annotation update)
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Last sequence update)
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
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01-APR-2004 (TERMBLEEL 27,
01-APR-2004 (TERMBLEEL 27,
01-APR-2004 (TERMBLEEL 27,
AGYD PROCEIN.
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Best Local Similarity 77.0-
7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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01-APR-2004 (TrEMBLrel.
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SEQUENCE FROM N.A.
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PROSITE; PS00311; LAMP 2; 1.
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Kancko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kchara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21664373; PubMed=11792842; Shintzu T., Ohenima K., Yamashita A., Shintzu T., Odeamai K., Hiztori M., Kuhara S., Hayashi H.; Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; AP005960; BAC52234.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
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0
                                                                                                                                                                                                                                                                                                                                                                                                                          Bradyzhizobium japonicum.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales;
Bradyzhizobiaceae, Bradyzhizobium.
VGCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.6%; Score 33; DB 2; Length 153; 77.8%; Pred. No. 15; 2; Indels tive 0; Mismatches 2; Indels
                                                       Score 33; DB 2; Length 47; Pred. No. 4.2; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 AA; 15488 MW; 23C7D464AA94A490 CRC64;
              22893764DF54BFA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TYEMBLrel. 20, Created)
01-MAR-2002 (TYEMBLrel. 20, Last sequence update)
01-UJN-2003 (TYEMBLrel. 24, Last annotation update)
Hypothetical protein CPE2505.
OrderedLocusNames=CPE2505;
                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
EMBL; AP002194; BAB82211.1; -.
GO; GO:0016020; C:membrane; IEA.
                                                                                                                                                                                                                                                                                    153 AA
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                                                       Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
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EMBL; AJ617719; CAE92757.1;
SEQUENCE 47 AA; 5149 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 77.00,
Best Local 7, Conservative
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                                                                                                                                                                                 GVNACSSLF 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GANAQASLF 81
                                                                                                                                        1 GVNAXASLF 9
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                                                                                                                                                                                                                                                                                                                                                                                      Blr6969 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=USDA110;
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(209EV1)
10 01-JU
DT 01-JU
DT
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KE STRAIN-EZECH 11;

KRAIN-EZECH 12;

KRAIN-EZECH 12;

KRAIN-EZECH 12;

KRAIN-EZECH 12;

KRAIN-EZECH 12;

KRAIN-EZECH 12;

KRAIN-EZECH 13;

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TISSUE-Mammary tumor metastatized to lung. Tumor arose spontaneously;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.6%; Score 33; DB 2; Length 463; 66.7%; Pred. No. 47; ive 2; Mismatches 1; Indels
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006785; AAH06785.1; -.
GO; GO:0005764; Lampl.
GO; GO:0005771; C:mltivesicular body; IDA.
GO; GO:00042383; C:sarcolemma; IDA.
InterPro; IPR002000; Lamp.
PF01299; Lamp.
GO, GO:0015297; F:antiporter activity; IEA.
GO; GO:0015238; F:drug transporter activity; IEA.
GO; GO:0006855; P:multidrug transport; IEA.
GO; GO:0006855; P:multidrug transport; IEA.
FIGREPMS; TIGR00795; MatE; 2.
FIGREPMS; TIGR00797; matE; 1.
Complete proteome; Hypotetical protein.
SEQUENCE 463 AA; 51100 MW; 6EE1B38S633DEEB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Last sequence update)
Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lamp1 protein (Fragment).
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Best Local Similarity 66.7
Matches 6; Conservative
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Search completed: October 26, 2004, 16:05:03 Job time: 42.6324 secs
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      FROM N.A.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
SI:zK83D9.1 (Novel protein similar to vertebrate aquaporin 3 (AQP3))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Fragment).
Name=S1:zKB1D9.1;
Name=S1:zKB1D9.1;
Burachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii, Neopterygii, Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
(VDEI_TAXID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Brugia.
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                                         Length 189;
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                                                                               1; Indels
71F16D69BA4066FA CRC64;
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SEQUENCE 259 AA; 30791 MW; 3A8EE64649880596 CRC64;
                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cytochrome c oxidase subunit III.
                                     Score 32; DB 2;
Pred. No. 32;
2; Mismatches
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Mitochondrion.
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PROSITE; PS50253; COX3; 1.
  20456 -MW;
                                     82.1%;
66.7%;
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tes 6; Conservative
                                                                           6; Conservative
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189 AA;
                                                                                                                   1 GVNAXASLF
                                     Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=6279;
                                                                                                                                                                                                                                                                                                                                                                               Name=cox3;
  SQ SEQUENCE
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Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.

Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.

-!-SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

-!-SIMILARIY: Belongs to the MIP/aquaporin (TC 1.A.8) family.

EMBL; AL84518; CAE56668.1; ---

R GO; GO:0005741; C:mitcohondrial outer membrane; IEA.

GO; GO:0015288; F:porin activity; IEA.

R GO; GO:005529; MIP; I.

Pfam; PRO0230; MIP; I.

R ProDon; PRO0359; MIP; I.

IGRAPAS; TIGRRO0861; MIP; I.

NOTIN: Transmembrane; Transport.
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
SI:zKB3D9.1 (Novel protein similar to vertebrate aquaporin 3 (AQP3))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Fragment).
S1:ZR3D9.1.
S1:ZR3D9.1.
Burachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygil; Neopterygil; Teleostel; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sehra H.;
Submitred (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AL844518; CAES0608.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                          263 AA; 28190 MW; 51D9D9594F03EA30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON TER 1 1 SEQUENCE 263 AA; 28190 MW; 51D9D9594F03EA30 CRC64;
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Best Local Similarity 66.7.
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Les 6, Conservative
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Protein e CpsiH pro H. pylori S. aureus

Aay67852 (Aams0900) Aams0900 Aams0900 Aams0900 Abg241179 Abg241179 Abg28937 Aay68937 Aay68959 Aay67857 Adj48883 Adj48883 Adj48883 Adj488890 Adj48890 Adj48980 Adj48890 Adj4890 Adj48890 Adj4890 Adj48890 Adj48800 Adj4

Cyclic pe S. aureus

AgrD-auto

Cyclic pe Novel hum

AgrD-auto Cyclic pe Novel hum

Listeria

Streptoco Oil-assoc Wheat fru Oil-assoc

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S. aureus peptide #6 used for bacterial interference
                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                       AAY67852
AAM50900
                                                                   ABP53541
ABG24179
ABG24179
ABG25396
AAY68973
AAY67857
AAM50005
AAM50005
AAM50005
ABB49861
ABB49861
ABB49861
ABP24863
ABP2486477
ABP2486477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-00103438
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 Staphylococcus aureus
Misc-difference
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 AAY67856;
AgrD2 lac
AgrD2 lin
AgrD2 lin
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Staphyloc
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                                                                                             October 26, 2004, 15:44:15 ; Search time 42.75 Seconds (without alignments) 75.522 Million cell updates/sec
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            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                    - protein search, using sw model
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AAY67860
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AAMS1002
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AAMS1005
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Gapop 10.0 , Gapext 0.5
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No.
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This sequence represents a cyclic peptide derived from the Staphylococcus aureus AgrD peptide. The invention relates to AgrD derived peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes New cyclic peptides for treating infections with Staphylococcus aureus /note= "N-terminal residue forms bond with C-terminal Staphylococcus aureus infection; cyclic peptide; AgrD; agr response; virulence factor; treatment. ď residue to form a cyclic peptide" છે ij Location/Qualifiers RP, Claim 9; Page 26; 37pp; English. Novick (UYRQ) UNIV ROCKEFELLER. (UYNY) UNIV NEW YORK STATE. TW, Mayville P, WPI; 2000-147202/13. Muir ANY CASE OF THE STATE TO ANY CASE OF THE STATE OF THE STA

S. aureus Staphyloc

Peptide-m AgrD2 lac

Protected AgrD-auto

AAM50908 AAM50899 ABP53540 AAM51001 ABB84631

Cyclic pe Transcrip

Agr̃D2 thi S. aureus

Abp53540 C Aw38323 T Abb07159 E Aam51011 A Adf98875 E Adf98875 E Abb84634 S Adf98975 E Adf99193 S

ADJ98875 ABB84634 ADF09193

aureus Peptide t

Peptide-m

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peptide involves: assembling a linear peptide chain on to a solid phase resin support; deprotecting the resulting protected assembled peptide; treating the deprotected peptide with neutral buffer for a time sufficient to form the cyclic peptide and cleave the peptide from the support; and recovering the cyclic peptide. The peptide is useful for bacterial interference, especially for the treatment of S. aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muir TW, Mayville P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New cyclic peptides,
infections.
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MAYVILLE P.
NOVICK R P.
BEAVIS R.
JI G.
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Best Local Similarity
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                                                                                                         Sequence 9 AA;
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24-JUN-1999;
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                                                                                  infection
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                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of a novel synthetic cyclic peptide of the invention that is capable of inhibiting the agr response of staphylococcus aureus. It is an AgrD-autoinducing peptide, where AgrD is a secreted agr-encoded peptide and where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. Preferred peptides may have the sequence NH2-X(n)-Z-X(y)-COGH, with a cyclic bond between the Z residue and COGH other than a thiosester bond, where X is an amino acid, an amino acid analogue, a peptidomimetic or non-amide isostere, Z is a synthetic or a biosynthetic amino acid, n is 0-10 and y is 1-10. The cyclic bond is especially a lactam or lactone bond. The thiololactone structure within native AgrD peptides is required for activation of the gruncture can destroy agr response activating activity while preserving and enhancing inhibitory activity. A claimed method of preparing a cyclic
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      with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus
                                                                                                                                                                                                                                                                                                                                                                                                           note= "note linked to residue 9 to form cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "note linked to residue 5 to form cyclic peptide"
                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                Staphylococcus aureus, AgrD; agr response, inhibitor; antibiotic; antibacterial; infection; therapy; cyclic.
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                                                                                                                                                                                                                                                                                          AgrD-autoinducing cyclic peptide, inhibitor of agr response.
                                                                    94.9%; Score 37; DB 3; Length 9; 100.0%; Pred. No. 1.7e+06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                              AAM50904 standard; peptide; 9 AA.
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(UYNY ) UNIV NEW YORK STATE.
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                                                        Query Match
Best Local Similarity luv.
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     with this
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                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cyclic peptide, Staphylococcus aureus, infection, antibacterial; agr response inhibitor.
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94.9%; Score 37; DB 5; Length 9; 100.0%; Pred. No. 1.7e+06; ive 0; Mismatches 0; Indels
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                                                         Conservative
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This sequence represents the Staphylococcus aureus AgrDII derived peptide. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of different group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus
                                                                                                                                                                                                                                                                                                   New cyclic peptides for treating infections with Staphylococcus aureus.
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Pred. No. 1.7e+06;
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(QUOR-) QUOREX PHARM INC.
(UYTE-) UNIV TECHNOLOGIES INT INC.
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(UYNY ) UNIV NEW YORK STATE.
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Best Local Similarity 77...
7; Conservative
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                              Staphylococcus aureus.
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.larity 77.8%; Pred. No. 1.7e+06;
Conservative 1; Mismatches 1; Indels
Indels
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                   Muir TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM51004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                            subject.
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                                                                                                                                                                     The invention relates to the use of autoinducer-2 (AI-2) agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis. Synergistic compositions comprising inhibitors of the quorum-sensing pathway of a microorganism are also provided. Methods using such AI-2 analogues are useful for treating pathogen-associated disease states. The compounds and antibiotic compositions can be used to inhibit bacterial cell growth and/or biofilm formation on a medical device, particularly for promoting growth of skin graft replacements used in the treatment of burns and ulcers. They may also be used to aid wound repair, and to inhibit bacterial cell growth and biofilm formation in or on products or devices used for personal hygiene. The present sequence represents a inhibitor of peptide-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "note linked to residue 9 to form cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "note linked to residue 5 to form cyclic peptide"
                                            use of autoinducer-2 agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis, also antibiotic compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic; antibacterial; infection; therapy; cyclic.
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Pred. No. 1.7e+06;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protected peptide used in cyclic peptide production.
                                                                                                                                        Disclosure; Page 33; 134pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "Ser(tBu)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "Ser(Bzl)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM50907 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "Ser(Bz1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Z-Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.78;
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(UYNY ) UNIV NEW YORK STATE.
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Best Local Similarity 77.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVNASSSLF 9
                 WPI; 2002-075235/10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                          quorum sensing
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9 AA;
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Modified-site
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AAMS 09907
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The present sequence is that of a protected peptide used in an example of the preparation of novel synthetic cyclic peptides of the invention (see AAM50899-906). The peptide corresponds to the Staphylococcus aureus AgrDII sequence with a Cyse to Ser mutation (lactone). It was synthesised on a Wang-resin using an Fmco N-alpha protection strategy. Following chain assembly, the peptide was cleaved from the support and the Ser-5 residue deprotected by treatment with a trifluoroacetic acidianisole:water mixture (90:5:5) for 4 hr. The partially protected peptide alpha carboxylates were then dissolved in DMF and treated with PMSOF and a catalytic amount of dimethylaminopyridine. Cyclitation was complete after 2 hr. The remaining protecting groups were then removed by treatment with HF and the peptide purified by HPLC. The cyclic peptide is capable of inhibiting the agr response of Staphylococcus aureus. The thiololactone structure within native AgrD peptides is required for activation of this response. Replacement of the thiol ester component of the cyclic ring structure with a lactone (as in the present case) or a lactam can desiroy agr response activating activity while preserving and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enhancing inhibitory activity. The cyclic peptides are useful for bacterial interference, especially for the treatment of S. aureus
                                                                                                                                                  Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in
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Beavis
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Novick RP,
                                                                                                                                                                                                                                                                                                 Disclosure, Col 14, 18pp, English.
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Mayville P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
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Synthetic.
                                                                           WPI; 2002-170774/22.
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Matches 7; Conserv
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AAM51002;
                                 subject.
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                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
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                                                                                     Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in
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Pred. No. 1.7e+06;
1; Mismatches 1; Indels
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                                           Beavis R,
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                                         Mayville P, Novick RP,
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                                                                                                                               Example 1; Col 9; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AgrD2 linear free acid peptide.
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative 1
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(UYNY ) UNIV NEW YORK STATE.
         (UYNQ ) UNIV ROCKEFELLER.
(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                       GVNASSSLF 9
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                                                               WPI; 2002-170774/22.
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                                                                                                                                                                                                                                                                                                                                                         Sequence 9 AA;
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                                         Muir TW,
                                                                                                           subject.
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The present sequence is that of a novel synthetic AgrD2 linear free acid peptide. The peptide is derived from the cyclic AgrD2 peptide of Staphylococous aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beal-lactamase reporter gene fused to the agr3 promoter. This allowed activation or inhibition of the agr response to be monitored spectrophotometrically. Unlike an AgrD2 thiololactone cyclic peptide (see AAM51001), the present peptide was unable to either activate or inhibit the agr response, even when added to cultured cells at Un concentrations. The invention provides claimed cyclic peptides (see AAM51091) and methods for preparing them. The cyclic peptides are useful for bacterial interference, especially for the creatment of S. aureus infection.
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Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.7%; Score 35; DB 5; L
77.8%; Pred. No. 1.7e+06;
iive 1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM51002 standard; peptide; 9 AA.
                                                                                                                        Example 1, Col 9, 18pp, English
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(UYNY ) UNIV NEW YORK STATE.
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Best Local Similarity 7/...
1, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Modified-site
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Gaps

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0: Indels

Score 34; DB 3; I Pred. No. 1.7e+06; 1; Mismatches 0;

87.2%; 88.9%;

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9 Length

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activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus
                                                                                                                Ouery Match
Best Local Similarity 80...
8, Conservative
                                                                                                                                                                                                                                     1 GVNAXSALF
                                                                                                                                                                                                                                                           |||||||||
1 GVNAXSSLF
                                                                                            Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY67861;
                                                                                                                                                                                                                                                                                                                                                     RESULT 12
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AAY6

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                                         The present sequence is that of a novel synthetic AgrD2 linear thioester peptide. The peptide is derived from the cyclic AgrD2 peptide of Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agrB3 promoter. This allowed activation or inhibition of the agr response to be monitored spectrophotometrically. Unlike an AgrD2 thiololactone cyclic peptide (see AAM51001), the present peptide was unable to either activate or inhibit the agr response, even when added to cultured cells at UM concentrations. The invention provides claimed cyclic peptides and aAAM50899-306 and AAM50899 and methods for preparing them. The cyclic peptides are useful for bacterial interference, especially for the treatment of S. aureus infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New cyclic peptides for treating infections with Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus infection; cyclic peptide; AgrD; agr response;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S. aureus peptide #1 used for bacterial interference.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beavis R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35; DB 5; L
Pred. No. 1.7e+06;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ji G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novick RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY67851 standard; peptide; 9 AA.
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    Example 1; Col 9; 18pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.7%;
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(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    virulence factor; treatment.
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Best Local Similarity 77.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-147202/13
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New cyclic peptides for treating infections with Staphylococcus aureus
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                                                                                                                                                                                                         Staphylococcus aureus infection; AgrD; agr response; treatment; virulence factor.
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                                                                                                                                                            Staphylococcus aureus AgrDII derived peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beavis R;
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AAY67861 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                     /label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US014562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-00103438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYRQ ) UNIV ROCKEFELLER.
(UYNY ) UNIV NEW YORK STATE.
                                                                                                         (first entry)
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Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                 Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muir TW, Mayville P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-147202/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUN-1999;
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                                                                                                         25-APR-2000
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(revised)
(first entry)

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AgrD2; agr response; inhibitor; antibiotic; antibacterial; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muir TW, Mayville P, Novick RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Col 11; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYRQ ) UNIV ROCKEFELLER.
(UYNY ) UNIV NEW YORK STATE.
                                                              AgrD2 lactam cyclic peptide.
                                                                                                                                                 Staphylococcus aureus. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-170774/22.
                                                                                                                                                                                                                                                   Misc-difference 5
                                                                                                                    therapy; cyclic.
                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                  Misc-difference
              07-AUG-2003
08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                       24-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUN-1998;
                                                                                                                                                                                                                                                                                                                                    US6337385-B1
                                                                                                                                                                                                                                                                                                                                                                      08-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subject.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to the use of autoinducer-2 (AI-2) agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis. Synergistic antibiotic compositions comprising inhibitors of the quorum-sensing pathway of a microorganism are also provided. Methods using such AI-2 analogues are useful for treating pathogen-associated disease states. The compounds and antibiotic compositions can be used to inhibit bacterial cell growth and/or biofilm formation on a medical device, particularly for promoting growth of skin graft replacements used in the treatment of burns and ulcers. They may also be used to aid wound repair, and to inhibit bacterial cell growth and biofilm formation in or on products or devices used for personal hygiene. The present sequence represents a inhibitor of peptide-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of autoinducer-2 agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis, also antibiotic compositions.
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                                                                                                                                                                            Autoinducer-2; AI-2; antibiotic; antibacterial; dermatological; vulnerary; pheromone; agr system; accessory gene regulator; cyclic.
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0
                                                                                                                                             Peptide-mediated quorum sensing inhibitor peptide cyclo-XIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stein J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.2%; Score 34; DB 5; Length 9;
88.9%; Pred. No. 1.7e+06;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                               /note= "diaminoprprionic acid residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shokat K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bassler BL, Dammel CS, Schauder S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 33; 134pp; English.
                                                                                                                                                                                                                                                     Location/Qualifiers
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYPR-) UNIV PRINCETON.
(QUOR-) QUOREX PHARM INC.
(UYTE-) UNIV TECHNOLOGIES INT INC.
                                            ABB07161 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0203000P
                                                                                                                                                                                                                                                                                                                                                                                                 10-MAY-2001; 2001WO-US015221
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                                                                                                                                                                                                                                                                Key
Modified-site
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                                                                                                           13-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAY-2000;
07-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                   15-NOV-2001
                                                                           ABB07161;
                                                                                                                                                                                                                                Synthetic
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Matches
          RESULT 13
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Beavis R,

/note= "note linked to residue 5 to form cyclic peptide"

'note= "any amino acid"

99US-00339511. 98US-0090402P

Location/Qualifiers 5

'note= "note linked to residue 9 to form cyclic peptide'

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The present sequence is that of a novel synthetic AgrD2 lactam cyclic peptide in which residue 5 of the peptide is linked to residue 9 via a clactam bond. The peptide is derived from an AgrD2 peptide 0 via a clactam bond. The peptide is derived from an AgrD2 peptide of staphylococous aurens group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agrs prometer. This allowed activation or inhibition of the agr response to be monitored spectrophotometrically. The AgrD3 lactam peptide inhibited the agr response in group I S. aureus strains and did not activate the agr response in group I S. aureus strains and did not activate the agr response in group I. II or III strains. The invention provides claimed cyclic peptides (see AAX/S0099-906 and AAX/S0099-006 and Amanowally for the treatment of S. aureus infection. (Updated on 07-AŭG-2003 to correct OS fileld.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 5; Length 9;
Pred. No. 1.7e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM50908 standard; peptide; 9 AA.
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Best Local Similarity 88.9
Matches 8, Conservative
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AAM50908
ID AAM50
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AAM51005 standard; peptide; 9 AA.

RESULT 14 AAM51005 AX B

AAM51005

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1 GVNAXSALF 1 GVNAXSSLF Search completed: October 26, 2004, 15:59:45 Job time: 43.75 secs

GVNAXSALF GVNAXSSLF

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The present sequence is that of a protected peptide used in an example of the preparation of novel synthetic cyclic peptides of the invention (see AAMS0899-906). The peptide corresponds to the Staphylococcus aureus AAMS089-906). The peptide corresponds to the Staphylococcus aureus AAMS089-906. The synthesised on a Wang-resin using an Fmoc N-alpha (lactam). It was synthesised on a Wang-resin using an Fmoc N-alpha protection strategy. Following chain assembly, the peptide was cleaved from the support and the Dpr-5 residue deprotected by treatment with a trifluoroacetic acid:anisole:water mixture (90:5:5) for 4 hr. The partially protecting operated alpha carboxylates were then dissolved in DMF and treated with PyBOP. Cyclization was complete after 2 hr. The remaining protecting groups were removed by treatment with HF and the peptide purified by HPLC. The cyclic peptide is capable of inhibiting the agr response of Staphylococcus aureus. The thiololactone structure within native AgrD peptides is required for activation of this response.

Replacement of the thiol ester component of the cyclic ring structure with a lactam (as in the present case) or a lactone can destroy agr response activating activity while preserving and enhancing inhibitory activity. The cyclic peptides are useful for bacterial interference,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activity. The cyclic peptides are useful for bacter
especially for the treatment of S. aureus infection
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                                                                                                                                                                                                                                     'note= "Z-Gly"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYNQ ) UNIV ROCKEFELLER.
(UYNY ) UNIV NEW YORK STATE.
                                              08-MAY-2002 (first entry)
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                                                                                                                                                                                                                                                     Misc-difference
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Modified-site
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                                                                                                                                                                    Synthetic
                AAM50908;
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Gaps

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0; Indels

87.2%; Score 34; DB 5; Length 9; 88.9%; Pred. No. 1.7e+06; tive 1; Mismatches 0; Indels

Query Match
Best Local Similarity 88.9
Matches 8; Conservative

Sequence . 9 AA;

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'note= "note linked to residue 9 to form cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "note linked to residue 5 to form cyclic peptide"
                                                       Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic; antibacterial; infection; therapy; cyclic.
Protected peptide used in cyclic peptide production.
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                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "Ser(Bzl)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "Ser(Bzl)"
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October 26, 2004, 15:54:00; Search time 31.5 Seconds (without alignments) 92.502 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                              1364641 segs, 323758627 residues
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Maximum Match 100%
Listing first 45 summaries
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                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                        US-10-032-950-6
39
1 GVNAXSALF 9
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                                                OM protein
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 40852. A	857,	12, A	Sequence 984, App	60718	equence 9222, A	equence 53	equence 12	574	Sequence 4, Appli	9	σ	4	Sequence 137791,	Seguence 7538, Ap	297	1617	Н	1280,	6493	$\overline{}$	189388	141, Ap	2080,	47541,	,727,		equence 12158,	44158	10	341,	a)
US-10-767-701-40	10-389-566-857	US-10-004-502-1	US-10-389-566-98	US-10-425-114-607	4 US-10-156-761-92	5 US-10-282-122A-530	US-10-369-493-	US-09-841-132-574	ĕ	24-599-2608	67-701-5904	24-599-143	37-963-1377	164-408A-753	67-701-5297	-701-6161	4-018-12	83-357-128	25-114-6493	82-122A-4565	37-963-1893	166-050A-1	64-237-208	5 US-10-282-122A-47	US-09-815-242-572	US-09-820-044	-09-815-242-1215	S US-10-282-122A-4415	0-282-122A-72	US-09-866-050A-3	0-004-378A-12
266	336	337	337	370	391	442	468	605	o	09	71	101	117	122	131	139	144	255	273	284	313	322	332	335	338	341	341	341	354	431	431
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14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	50	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Sequence 6, Application US/10032950
| Publication No. US20020077453A1
| GENERAL INFORMATION. US20020077453A1
| APPLICANT: Mayville, Patricia
| APPLICANT: Deavis, Rohad
| TITLE OF INVENTION: UNMER: US/10/032,950
| TURENT FILING DATE: 2001-12.27
| PRIOR PILING DATE: 2001-12.27
| PRIOR PILING DATE: 2001-12.27
| PRIOR PILING DATE: 1998-06-24
| NUMBER OF SEQ ID NOS: 8
| SOFTWARE: PATRICIAN SEQUENCE | SOFTWARE: PATRICIAN DESCRIPTION OF ARTIficial Sequence | FRATURE: OTHER INFORMATION: Description of Artificial Sequence | FRATURE: OTHER INFORMATION: Peptide | OTHER INFORMATION: Peptide | OTHER INFORMATION: Axa represents any amino acid at this position. US-10-032-950-6 | OTHER INFORMATION: Yellow | OTHER Yellow | OT
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1 GVNAXSALF 9

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APPLICATION OF JO201444

Sequence 6, Application US/10201444

Sequence 6, Application US/10201444

Publication No. US20030078378A1

GENERAL INFORMATION:

APPLICANT: New York University Medical Center

TITLE OF INFUNTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS

FILE REFERENCE: 63753/7

CURRENT FILING DATE: 2002-07-23

PRIOR APPLICATION NUMBER: US/08/861,476

PRIOR APPLICATION NUMBER: US/08/861,476

PRIOR APPLICATION NUMBER: US/08/861,476

PRIOR APPLICATION NUMBER: 3997-05-22

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin version 3.0

SEQ ID NO 6

SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/10032950
; Sequence 5, Application No. US20020077453A1
; Publication No. US20020077453A1
; GENERAL INPORMATION:
APPLICANT: Mayville, Parricia
APPLICANT: No. US2002007453A1ick, Richard P.
APPLICANT: Of US2002007453A1ick, Richard P.
APPLICANT: No. NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION NUMBER: US/10/032,950
CURRENT FILING DATE: 1998 06-24
; RICHARDAR APPLICATION NUMBER: 60/090,402
; PRIOR FILING DATE: 1998 06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
GGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
NAME/KEY: VARIANT
LOCATION: (5)
OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33; DB 14; Length 47;
Pred. No. 3.8;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-201-444-6
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Best Local Similarity 77.8%;
Matches 7; Conservative
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1 GVNAXASLF 9
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Matches 7; Conserv
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Publication No. US20030078378A1

GENERAL INFORMATION:
APPLICANT: New YORK University Medical Center
TITLE OF INVERTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
FILE REFERENCE: 63753/7

CURRENT PELING DATE: 10970201,444

CURRENT FILING DATE: 109708/861,476

PRIOR APPLICATION NUMBER: US/08/861,476

PRIOR PED IN OS: 8

SOFTWARE: Patentin version 3.0

SEQ ID NO 3
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                                                                                                                                                                       Sequence 1, Application US/10032950
; Publication W. US20020077453A1
; RUBLICARIA INFORMATION:
; APPLICANT: Mulr, Tom
; APPLICANT: Mayville, Patricia
; APPLICANT: Mayville, Patricia
; APPLICANT: No. US20020077453A11ck, Richard P.
; APPLICANT: No. WOUSLE STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
; APPLICANT: Ji, Guangyong
; TITLE OF INVENTION: INTERERENCE
; TITLE OF INVENTION: INTERFERENCE
; TITLE OF INVENTION: INTERFERENCE
; FILE REFERENCE: 600-1-231N
; CURRENT APPLICATION NUMBER: 60/090,402
; PRIOR APPLICATION NUMBER: 60/090,402
; PRIOR APPLICATION NUMBER: 60/090,402
; RILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; FROM TO COMMENT PATRICIAL PATRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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88.9%; Pred. No. 1.2e+06;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.6%; Score 33; DB 14; Length 9; 77.8%; Pred. No. 1.2e+06; Live 1; Mismatches 1; Indels
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; ORGANISM: Staphylococcus aureus
US-10-201-444-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
1 GVNAXSALF 9
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US-10-369-493-19084
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US-09-767-041-33
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APPLICANT: Carr, Grant
APPLICANT: Carr, Grant
APPLICANT: Carr, Grant
APPLICANT: Torsyth, R.
APPLICANT: APPLICANT: APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPRENCE: ELITRA, 0.94
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PAPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-66
PRIOR FILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-110-23
APPLICANT: May lle, Patricia
APPLICANT: May lle, Patricia
APPLICANT: May lle, Patricia
APPLICANT: No. 192002007453Alick, Richard P.
APPLICANT: No. 19202007453Alick, Richard P.
APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: LTTERFERENCE
FILE REFERENCE: 600-1-231N
CURRENT FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR PILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.9%; Score 30; DB 13; Length 9; larity 77.8%; Pred. No. 1.2e+06; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-282-122A-53320
; Sequence 53320, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Foreyth, R.
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1 GANAXSSLF 9
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Best Local Similarity
Matches 7; Conserv
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APPLICANT: Li, Ping TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFREENCE: 38-21(5321) B CURRENT APPLICATION NUMBER: US/10/437,963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Li, Ping Transport of the Molecules and Other Molecules Associated With TITLE OF INVEXMION: Rice Nucleic Acid Molecules and Other Molecules Associated With FILE REPERENCE: 38-21(33221)B CURENT APPLICATION NUMBER: US/10/437,963 CURENT APPLICATION NUMBER: 12003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 113791
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                                                                                                                                                    ; LOCATION: (5)
; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-7
                        TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION:
NAME/KEY: VARIANT
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Pred. No. 18+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                  Score 29; DB 13; Length 9;
Pred. No. 1.2e+06;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT4530_17545C.1.pep
US-10-437-963-113791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 113791, Application US/10437963
Publication No. US20040123343A1
GENERAL INPORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: (ao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 144131, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boukharov, Andrey A.
Barbazuk, Brad
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 66."

"There is Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                         1 GVNAXSALF 9
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41 GLRAASALF
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APPLICANT:
APPLICANT:
      LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 184, Application US/0988227
Publication No. US20030158396A1
GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold
APPLICANT: Al-Garawi, Amal
APPLICANT: Miler, Charles
APPLICANT: Ocomen, Raymond P.
TITLE OF INVENTION: Encoding No. US20030158396A1e1 Helicobacter Polypeptides in the
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/047002
CURRENT APPLICATION NUMBER: US/09/882,227
CURRENT FILING DATE: 1001-06-15
PRIOR FILING DATE: 1001-06-15
PRIOR PILING DATE: 1007-07-29
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Publication No. US20020077453A1
GENERAL INPORMATION:
APPLICANT: Muir, Tom
APPLICANT: No. US20020077453A1ick, Richard P.
APPLICANT: No. US20020077453A1ick, Richard P.
APPLICANT: No. US20020077453A1ick, Richard P.
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
CURRENT APPLICATION NUMBER: US/10/032,950
CURRENT FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
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                                                                                                                                                                                                Length 508;
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Pred. No. 2.7e+02;
2; Mismatches 2; Indels
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                                                                                                                                                                                            Score 30; DB 14;
Pred. No. 2.5e+02;
1; Mismatches 1;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 184
LENGTH: 549
      60/360,039
; PRIOR APPLICATION NUMBER: US 60,
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 19084
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Anabaena PCC7120
US-10-369-493-19084
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55.6%;
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75.0%;
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, ORGANISM: Helicobacter pylori
US-09-882-227-184
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
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Best Local Similarity 55.6
Matches 5; Conservative
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Best Local Similarity
Matches 6, Conserva
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US-10-389-566-857

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RESULT 14
US-10-767-701-40852
is Sequence 40852. Application US/10767701
is Publication No. US20040172684A1
is GENERAL INFORMATION:
APPLICANT: Cavouric, David K.
is APPLICANT: Zhou, Yihua
is APPLICANT: Cavo, Yongwei
is TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
it TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
is FILE REFERENCE: 38-21(53535)B
is CURRENT APPLICATION NUMBER: US/10/767,701
is CURRENT FILING DATE: 2004-01-29
is NUMBER OF SEQ ID NOS: 63128
is SEQ ID NO 40852
in LENGTH: 266
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Publication No. US20040025202A1

GENERAL INFORMATION:

APPLICANT: Laurie, Cathy C

TILLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants

FILE REFERENCE: 38-77(52900) D

CURRENT FILING DATE: 2003-03-31

PRIOR PILING DATE: 2002-03-15

PRIOR FILING DATE: 2002-03-15

PRIOR FILING DATE: 2002-03-16

PRIOR FILING DATE: 2002-06-25

PRIOR FILING DATE: 2002-06-25

PRIOR FILING DATE: 2002-06-26

PRIOR FILING DATE: 2002-06-26

NUMBER OF SEQ ID NOS: 2459

SOFTWARE: Patentin version 3.2

LENGTH. 100 857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C105350_1.pep
US-10-767-701-40852
                                                                                                                                                         CTHER INFORMATION: Clone ID: PAT_MRT4530_44976C.1.pep US-10-437-963-144131
TYPE: PRT ORGANISM: Triticum aestivum
                                                                                                                                                                                                                      Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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193 GVEAAALF 201
                                                                                          TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                                                                                                        140 WASSAVF 147
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US-10-389-566-857
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Query Match
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Bast Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GVNAKSALF 9
Db 89 GVNAEGCLF 97
Search completed: October 26, 2004, 16:10:13
Job time: 32.5 secs
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us-10-032-950-6.rpr

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 26, 2004, 15:46:55; Search time 8.73529 Seconds (without alignments) 99.132 Million cell updates/sec Run on:

US-10-032-950-6 39 1 GVNAXSALF 9 Title: Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Agrb protein [impo	somal mem	P2B/LAMP-1 precurs		ferrichrome ABC tr	manganese transpor	alpha-mannosidase	ferric exochelin u	hypothetical prote	hypothetical prote	2,3-bisphosphoglyc	conserved hypothet	hypothetical prote	PhnP protein [impo	flagellar biosynth	flagellar biosynth	transcription fact	probable galactosy	probable flagellar	receptor-protein k	aminopeptidase (BC	dase	ď	a]	cal	memb	g	Ϊ.	hypothetical prote
			C89995	A28067	A60534	A30200	C69812	AF2539	T30525	S60885	T22250	AD3198	AG2328	F64640	G84041	AB0421	AD1159	AD1518	S58439	54	H71562	7	9	T30942	422	\$20039	304	97	761	H75481	3
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hypothetical prote	glycoprotein endop	psD protein - B	probable polysacch	-chlorobenzoate	DNA-binding protei	NADH2 dehydrogenas	cholesterol oxidas	peptidase (M3 fami	phosphotransferase	protein Y32F6A.3	hypothetical prote	probable transcrip	hypothetical prote	SEC24 protein -	genome polyprote:
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966685	F69786	836653	E81286	F64053	WMBE42	D95366	A32260	F81313	D69750	G89189	T39530	846706	874291	548463	RRWPTM
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341	346	389	394	452	488	491	546	573	631	655	803	832	870	926	1844
71.8	71.8	71.8	71.8	71.8	71.8	71.8	71.8	71.8	71.8	71.8	71.8	71.8	71.8	71.8	71.8
28	28	28	28	28	58	28	28	28	28	58	28	28	28	28	28
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 Graphy protein [imported] - Staphylococcus aureus (strain N315) C, Species: Staphylococcus aureus C, Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004 C, Accession: C89995 R, Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguk R, Kuroda, M.; Ohta, T.; Wobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C, Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001 A, Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A, Reference number: A89758; MUD:21311952; PMID:11418146 A, Rocession: C89995 A, Molecule type: DNA A, Residues: 1-47 < KUR> A, Molecule type: DNA A, Residues: 1-47 < KUR> A, Residues: 1-47 < KUR> A, Residues: 1-47 < KUR> A, Residues: Strain N315 C, Genetics: A, Gene: agrD Query Match Query Match	Ouery Match 84.6%; Score 33; DB 2; Length 47; Best Local Similarity 77.8%; Pred. No. 0.81; Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps	1 GVMAXSALF 9
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24 GVNACSSLF 32 셤

A28067

lysocomal membrane glycoprotein LAMP-1 - mouse
CiSpecies: Mus musculus (house mouse)
CiAccession: A28667
R;Chen, J.W.; Cha, Y.; Yuksel, K.U.; Gracy, R.W.; August, J.T.
R;Chen, J.W.; Cha, Y.; Yuksel, K.U.; Gracy, R.W.; August, J.T.
R;Chen, J.W.; Cha, Y.; Yuksel, K.U.; Gracy, R.W.; August, J.T.
A;Chen, J.W.; Cha, Y.; Yuksel, K.U.; Gracy, R.W.; August, J.T.
A;Chen, J.W.; Cha, Y.; Yuksel, K.U.; Gracy, R.W.; August, J.T.
A;Reference number: A28067; MUD:88243732; PMID:3379044
A;Accession: A28067
A;Accession: A280

Gaps ; 0 Query Match
82.1%; Score 32; DB 2; Length 382;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 1; Indels

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99 GVNAGASLF 107
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es 6; Conserv
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Matches
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P2B/LAMP-1 precursor - mouse
P2B/LAMP-1 precursor - mouse
P2B/LAMP-1 precursor - mouse
P2B/LAMP-1 precursor - mouse
C;Species: Mas musculus (house mouse)
C;Species: Mas musculus (house mouse)
C;Accession: A60534
R;Heffernan, M.; Yousefi, S.; Dennis, J.W.
Cancer Res. 49; 6077-6084, 1989
A;Title: Molecular characterization of P2B/LAMP-1, a major protein target of a metastasi A;Reference number: A60534
A;Reference number: A60534
A;Steus: preliminary
A;Molecule type: mRNA
A;Residues: 1-405 AHRPA
A;Resi
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A; Residues: 1-407 < HOM>
A; Cross-reneces: UNIPROT: P14562; EMBL: J03672
A; Note: the authors translated the codon GGG for residue 15 as Val
R; Himeno, M.; Noguchi, Y.; Sasaki, H.; Tanaka, Y.; Furuno, K.; Kono, A.; Sakaki, Y.; Kat
PEBS Lett. 244, 351-356, 1989
A; Title: Isolation and sequencing of a cDNA clone encoding 107 kDa sialoglycoprotein in
A; Reference number: S03331; MUID: 89153580; PMID: 2920835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule type: mRNA
A,Residues: 22-407 cHIM>
A,Residues: 22-407 cHIM>
A,Cross-references: EMBL:X14765; NID:956577; PIDN:CAA32873.1; PID:956578
A,Note: part of this sequence, including the amino end of the mature protein, was confir
C,Superfamily: lysosome-associated membrane protein
C,Keywords: glycoprotein; membrane protein
F;22-407/Froduct: lysosomal membrane glycoprotein, 107K #status experimental cMAT>
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A;Title: Derived protein sequence, oligosaccharides, and membrane insertion of the 120-k glycoproteins.
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NyAlternate names: sialoglycoprotein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Oct-1989 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: A30200; S03331
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Pred. No. 13;
2; Mismatches 1; Indels
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C;Superfamily: lysosome-associated membrane protein
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Best Local Similarity 66.7
Matches 6; Conservative
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GMNATSSLF 289
                                                |:|| |:||
256 GMNASSSLF 264
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1 GVNAXSALF 9
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C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Accession: C6812
R;Kunst. F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C;Accesion: C6812
R;Kunst. F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Broullet, S.; Bruschi, C.V.; Callwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.; Bruschi, C.V.; Entian, W.D.; Errington, J.; Fabret, C.; Ferrari, E.
A;Authors: Foulgar, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A,Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maradia, R.; Maradori, J.; Barrot, B.; Roche, B.; Roche, B.; Roche, M.; Sadaie, Y.; Scanlon,
A,Authors: Schleich, S.; Schoeter, R.; Scoffone, F.; Sekiguchi, J.; Sckowska, A.; Scanlon,
A,Authors: Schleich, S.; Schoeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Scanlon,
A,Authors: Voshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Uchiyama,
A;Authors: Voshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Attle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Accession: C69812
A;Acussion: C69812
A;Acussion: C69812
A;Acussion: Preparation not shown; translation not shown
A;Molecule type: DMA.
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C; Species: Nostoc sp. PCC 7120
C; Species: Nostoc sp. PCC 7120
C; Species: Nostoc sp. PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C; Accession: AF2339
B; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchii Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; MUID:21595285; PMID:11759840
A; Accession: AF2539
A; Accession: AF2539
A; Residucule type: DNA
A; Residucule type: DNA
A; Residucule type: DNA
A; Residucule type: LNA
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C;Superfamily: natural resistance-associated macrophage protein
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Pred. No. 18;
2; Mismatches
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Pred. No.
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C;Superfamily: ferrichrome ABC transporter
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ilarity 66.7%;
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Best Local Similarity 66.7-
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alpha-mannosidase (EC 3.2.1.24) - Emericella nidulans

ferrichrome ABC transporter (permease) homolog yfmD - Bacillus subtilis

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A;Cross-references: UNIPROT:QSUKIO; GB:AE008687; PIDN:AAL46002.1; PID:g17743757; GSPDB:CS.A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: fepp
                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Rocidues: 1-533 < CUUR>
A;Crost-references: UNIPROT:08YPL2; GB:BA000019; PIDN:BAB75881.1; PID:g17133317; GSPDB:
A;Experimental source: strain PCC 7120
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  Length 298;
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                                                      Indels
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C,Superfamily: cofactor-independent phosphoglycerate mutase
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Pred. No. 51;
1; Mismatches
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Pred. No. 34;
1; Mismatches
        7
  Score 30; DB
Pred. No. 28;
1; Mismatches
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Best Local Similarity 75.0%;
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ilarity 75.0%;
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122 GVNAGAAFF 130
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Best Local Similarity
Matches 6; Conserv
     Query Match
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A;Molecule type: DNA
A;Residues: 1-361 <KUR>
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C;Species: Emericella nidulans, Aspergillus nidulans
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
E;Edecession: 10-33, 1998
A;Title: 16entification and analysis of a class 2 alpha-mannosidase in Aspergillus nidul
A;Reference number: 220843; MUID:98119762; PMID:9451011
A;Accession: T30525
A;Accession: T3052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ferric exochelin uptake protein fxuC - Mycobacterium smegmatis (fragment)
C.Species: Mycobacterium smegmatis
C.Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C.Accession: S60885
R.Fiss, E.H.; Yu, S.; Jacobs Jr., W.R.
Mol. Microbiol. 14, 557-569, 1994
A.Pitle: Identification of genes involved in the sequestration of iron in mycobacteria: A.Reference number: S60885, MUID:95191405, PMID:7885234
A.Residues: 1-234 <FIS>
A.Residues: 1-234 <FIS>
A.Cross-references: UNIPROT:Q50375; EMBL:U10425; NID:g595400; PIDN:AAC43258.1; PID:g5954
C.Genetics:
A.Gene: fxuC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-298 <WIL>
A;Cross-references: UNIPROT:Q93727; EMBL:Z78420; PIDN:CAB01709.1; GSPDB:GN00019; CESP:P4
A;Experimental source: clone F45H11
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22250
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. 60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rikelly, P. submitted to the EMBL Data Library, August 1996 A; Aceference number: 219537 A; Acession: T22550 A; Acetus: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: D...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.5%; Score 31; DB 87.5%; Pred. No. 60; ative 0; Mismatches
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A,Introns: 52/3; 109/2; 177/3; 248/1; 290/3
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Best Local Similarity 55.0.
Best Local Si Conservative
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Matches 7; Conservative
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37 GINSGAALF 45
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A;Gene: phnP
C;Superfamily: ATP-binding protein PhnP (PhnP)
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Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                       165 GLSADSALF 173
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                                                                                                            Query Match
Best.Local Similarity
Matches 6, Conserv
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C, Genetics
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                                  Cispecies: Helicobacter pylori
Cispecies: Malte, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: F64640
A;Accession: F64640
A;Accession: Preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Cross-references: UNIPROT:025619; GB:AE000605; GB:AE000511; NID:g2314103; PIDN:AAD0801
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AB0421
Phup protein [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Species: Versinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB0421
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
R;Parkhill, J.; Wren, B.W.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davies, P.; Dougan, G.;
Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 323-527, 2001
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Recession: AB0421
A;Recession: AB0421
A;Residues: preliminary
A;Residues: 1-250 «KUR>
A;Residues: 1-250 «KUR>
A;Cross-references: UNIPROT:Q82BF1; GB:AL590842; PIDN:CAC92694.1; PID:g15981389; GSPDB:G
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G84041

G84041

C94041

Cypothetical protein BH3135 [imported] - Bacillus halodurans (strain C-125)

C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: G84041

R;Takami, H: Massone, K: Fakki, Y: Masson, G: Sasaki, R: Masui, N: Fuji, F: Hirra Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Accession: G84041

A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-188 <STO>
A;Cross-references: UNIPROT:Q9K871; GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BAB068
A;Experimental source: strain C-125
C;Genetics:
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Best Local Similarity 55.6
Matches 5; Conservative
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es 6; Conservative
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Gaps

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Indels

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Cipgeries: Listeria monocytogenes
Cipate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
Cipate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
Cipate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
Cipacesion: AD1159
Riglaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A;Title: Comparative genomics of Listeria species.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: AD1159
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: Cala>
A; Molecule type: Loss GLA>
A; Experimental source: Strain EGD-e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          flagellar biosynthesic protein FliP homolog lmo0676 [imported] - Listeria monocytogenes
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                                                                                      Gaps
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0
    Length 250;
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Pred. No. 41;
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C,Superfamily: flagellar biosynthetic protein flip
n 74.4%; Score 29; DB Similarity 66.7%; Pred. No. 40; 6; Conservative 2; Mismatches
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Title: Perfect score: Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Result

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08ypl2 anabeens sp
025619 helicobacte
06faua acinecobacte
06gul2 xenopus lae
093ug agrobacteri
070106 convolvulus
cad92465 convolvulus
Cad92465 convolvulus
09c871 bacillus ha
09c871 bacillus ha
08c871 yarrowia li
08c861 yersinia pe
Aas60867 yersinia
092dx7 listeria in
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STRAIN=GUSICE C.)

GOGGING

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Ji G., Bearis R., Novick R.P.;
"Bacterial interference caused by autoinducing peptide variants.";
Science 276:2027-2030(1997).
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Last annotation update)
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Name=agrD; OrderedLocusNames=SAV2037;
Staphylococcus aureus (strain Mu50 / ATCC 700699).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus.
Bacteria, Firmicutes, Bacillales, Staphylococcus.
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Pred. No. 5.7;
1; Mismatches
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                GPMI ANASP
025619
025619
06GN12
093UY8
070L06
CAD92465
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Q8ZBF1
AAS60887
Q92DX7
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Best Local Similarity 77.0
7, Conservative
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 PRELIMINARY;
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SEQUENCE FROM N.A.
000000044444444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1280;
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01-JAN-1998 (
01-OCT-2004 (
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Name=agrD;
 Q7A2N4
Q7A2N4;
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Q7A2N4
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033586
 SCHOOLS
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O96011 leptospira
O96011 leptospira
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Q8xm78 clostridium
Q8etk0 oceanobacil
Q7d3d6 agrobacteri
Q8uk10 agrobacteri
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                                                                                                              October 26, 2004, 15:44:50; Search time 40.6324 Seconds (without alignments) 127.445 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                       1825181 seqs, 575374646 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LMP1_MOUSE
Q8VH34
LMP1_RAT
Q9DC13
Q7P724
Q7P724
Q6FB76
GPDA_SYNEL
GFB76
GPDA_SYNEL
G72NG2
MNTH_ANASP
Q72NG2
Q8FBN1
AAST1586
                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                  - protein search, using sw model
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Q7A417
CAE92745
CAE92751
CAE92754
CAE92757
Q9F1U5
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050375
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07D3D6
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Gapop 10.0 , Gapext 0.5
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2: uniprot_trembl:*
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Match Length
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Gaps

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47 AA.
                   PRELIMINARY;
RESULT 4
CAE92745
ID CAE92745
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SEQUENCE FROM N.A.

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CAE92745;
01-APR-2004 (TrEMBLrel. 27,
01-APR-2004 (TrEMBLrel. 27,
01-APR-2004 (TrEMBLrel. 27,
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CAE92748
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                                                                 MEDLINE-21311952; PubMed=11418146;
MEDLINE-21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba Thattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
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Pred. No. 5.7;
1; Mismatches 1; Indels
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Name=agrD; OrderedLocusNames=SA1842.1; ORFNames=SASO66;
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Last annotation update)
Bacteria, Firmicutes, Bacillales, Staphylococcus.
NCBI_TaxID=158878,
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Bacteria, Firmicutes, Bacillales, Staphylococcus.
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EMBL, AR003364; BAR58199.1; -.
InterPro; IPR00929; AgrD.
Pfam; PF0S931; AgrD; 1.
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Best Local Similarity 77.8%;
Matches 7; Conservative
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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EMBL, AP003135; BAB43124.1;
InterPro, IPR009229; AgrD.
Pfam; PF05931; AgrD; 1.
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7; Conservative
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SEQUENCE 47 AA;
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STRAIN-gran-cops,
Goerke C., Jasbach S., Kuemmel M., Wolz C.;
Goerke C., Dasbach S., Kuemmel M., Wolz C.;
Goerke C., Dasbach S., Kuemmel M., Wolz C.;
Goerke C., Bobbach S., Kuemmel M., Wolz C.;
Goerke C., Bobbylococcus aureus.";
and cap in Staphylococcus aureus.";
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
SERUL: AJ617715; CABS2745.1; -.
SEQUENCE 47 AA; 5149 MW; 22893764DFS4BFA7 CRC64;
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STRAIN=GELLB-CD5,
GOORNEC., DasBach S., Kuemmel M., Wolz C.;
"Evolutionary Models for the Development of the Polymorphic Loci agr and cap in Staphylococcus aureus.";
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ617716; CARE9274811. --
SEQUENCE 47 AA; 5149 WW; 22893764DF54BFA7 CRC64;
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Pred. No. 5.7;
1; Mismatches 1; Indels
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                                                                                                                   Bacteria, Firmicutes; Bacillales, Staphylococcus.
NCBI_TaxID=1280;
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
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CAE92751;
01-APR-2004 (TEMBLrel. 27,
01-APR-2004 (TEMBLrel. 27,
01-APR-2004 (TEMBLrel. 27,
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Best Local Similarity 77.8-
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Best Local Similarity 77.8
Matches 7; Conservative
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TISSUE-Mammary tumor metastatized to lung. Tumor arose spontaneously;

X TISSUE-Mammary tumor metastatized to lung. Tumor arose spontaneously;

X Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X Expleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

X Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

X Brownstein M.J., McKernan K.J., Malek J.A., Gunstathe P.H.,

X Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

X Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

X Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

X Hilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

X Blakesiey R.W., Touchman J.W., Green E.D., Dickson M.C.,

X Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
                                                                                                                                                                                                                                                                                   N. [1] —
SEQUENCE FROM N.A.
ARA Takeuchi S., Maeda T., Hashimoto N., Imaizumi K., Kaidoh T.,
RA Takeuchi S., Maeda T., Hashimoto N., Imaizumi K., Kaidoh T.,
RA Hayakawa Y.,
RT "Variation of the agr locus in Staphylococcus aureus isolates from cows with mastitis.";
RI "Ver. Microbiol. 79:267-274(2001).
RL Vet. Microbiol. 79:267-274(2001).
BMBL, AB043554; BAB16547.1; -.
DR EMBL, AB043554; BAB16547.1; -.
DR Pfam; PF05931; AgrD; 1.
SEQUENCE 46 AA; 5050 MW; 404714CDC4BFA77E CRC64;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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Last sequence update)
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Last sequence update)
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Bacteria, Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
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Pred. No. 9.6;
0; Mismatches
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2004 (TrEMBLrel. 26,
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Best Local Similarity 77.8
Matches 7; Conservative
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Name=Lampl;
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Q922T9
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Goerke C., Dasbach S., Kuemmel M., Wolz C.;
Goorke C., Dasbach S., Kuemmel M., Wolz C.;
"Boolutionary Models for the Development of the Polymorphic Loci agr and cap in Staphylcococus aureus.";
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, A.617718; CAR92754.1;
SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;
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STRAIN=gtll-cp8;
STRAIN=gtll-cp8;
STRAIN=gtll-cp8;
STRAIN=gtll-cp8;
STRAIN=gtll-cp8;
STRAIN=gtll-cp8;
Submittenary Models for the Development of the Polymorphic Loci agr and cap in Staphylococcus aureus.";
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ617719; CAE927571; -.
SEQUENCE 47 AA, 5149 NW; 22893764DF54BFA7 CRC64;
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          Goerke C., Dasbach S., Kuemmel M., Wolz C.;
"Evolutionary Models for the Development of the Polymorphic Loci agr and cap in Staphylococcus aureus.";
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AJG17717; CAE927511; -.
SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;
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Bacteria, Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
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Pred. No. 5.7;
1; Mismatches
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Pred. No. 5.7;
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Best Local Similarity 77.8
Matches 7; Conservative
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Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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CAE92754
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Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMP1 MOUSE STANDARD; PRT; 406 AA.
P11438; Q62020;
01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 15, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Lysosome.associated membrane glycoprotein 1 precursor (LAMP-1) (LGP-A) (LGP-120) (CD10.74) (P2B).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE=Brain;
MEDLINE=238825; Pubmed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeoberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Hang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Broask S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                                  FISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=90307738; PubMed=2142158;
Granger B.L., Green S.A., Gabel C.A., Howe C.L., Mellman I.,
                                                                                                                                                                                                                                                                                                                                                        82.1%; Score 32; DB 2; Length 189; 66.7%; Pred. No. 43; 1; Indels tive 2; Mismatches 1; Indels
                                                                                                                           Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006785; AAH06785.1;
MGD; MGI:96745; Lampl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heffernan M., Yousefi S., Dennis J.W.;
Submitted (FEB-1990) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                              189 AA; 20456 MW; 71F16D69BA4066FA CRC64;
                                             and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                       GO; GO:0005764; C:lysosome; IDA.
GO; GO:000577; C:multivesicular body; IDA.
GO: GO:0042383; C:sarcolemma; IDA.
InterPro; IPR002000; Lamp.
PF01299; Lamp; 1.
                                                                                                                                                                                                                                                                 PRINTS; PR00336; LYSASSOCTDMP.
PROSITE; PS00310; LAMP_1; 1.
PROSITE; PS00311; LAMP_2; 1.
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Matches 6; Conservative
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GMNASSSLF 71
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SEQUENCE
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RA Heleni
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RA Heffer
RN (3)
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RA Heffer
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Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mniting M., Madan A., Young A.C., Shevchenko Y., Bourfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
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MEDLINES 90237040. PubMed=2332434.
ARDALINES 90237040. PubMed=2332434.
Arterburn L.M., Earles B.J., August J.T.,
"The disulfide structure of mouse lysosome-associated membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lysosome-associated membrane glycoprotein
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 25-406 FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=88243732; PubMed=3379044;
Chen J.W., Cha Y., Yuksel K.U., Gracy R.W., August J.T.;
"Isolation and sequencing of a cDNA clone encoding lysosomal membrane glycoprotein mouse LAML. Sequence similarity to proteins bearing onco-differentiation antigens.";
J. Biol. Chem. 263:8754-8758(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i-FUNCTION: presents carbohydrate ligands to selectins. Also implicated in tumor cell metastasis.
-i-SUBCELLUAR LOCATION: Type I membrane protein. Lysosomal. This protein shuttles between lysosomes, endosomes, and the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  membrane.
-!- PTM: O- and N-glycosylated; some of the N-glycans attached to
LTMP-1 are polylactosaminoglycans (By similarity).
-!- SIMILARITY: Belongs to the LAMP family.
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                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Second lumenal domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMEL, BC049097; AAH490971; P. EMEL, J03881; AAA34411.1; P.R. A28067; A28067; P.R. A60534; A60531; Ampl. TherPro; IPRO(2000; Lamp. FROILS9; Lamp; P. PROSITE; PRO(310; LAMP. 1; 2. PROSITE; PS00310; LAMP. 2; 1.
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EMBL; M25244; AAA39869.1; -.
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N-linked (GlCNAC. ..) (Potential).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                       1; Indels
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AXO69968; Lamp1.
MOD; MOI:96745; Lamp1.
GO; GO:0005771; C:multivesicular body; IDA.
GO: GO:0005733; C:multivesicular body; IDA.
GO:0005733; C:multivesicular body; IDA.
FEMP: PPP1299; Lamp1.
FEMP: PPP1299; Lamp1.
                                                                                                                                                                                                                       7 -> IP (in Ref. 4).
-> I (in Ref. 2 and 4).
C1BD373548BB9655 CRC64;
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43879 MW; C1BD373548ADFA85 CRC64;
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Last annotation update)
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Pred. No. 98;
2; Mismatches
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PROSITE, PS00310, LAMP_1, 2.
PROSITE, PS00311, LAMP_2, 1.
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                                                                                                                                                                                                                                                                                                       6; Conservative
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Matches 6; Conser
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2219
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2222
282
282
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CARBOHYD
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CONFLICT
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                                                                                                                                                                                              "Derived protein sequence, oligosaccharides, and membrane insertion of the 120-kba lysosomal membrane glycoprotein (lgp120): identification of a highly conserved family of lysosomal membrane glycoproteins."; proc. Natl. Acad. Sci. U.S.A. 85:7577-7581(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lysosome-associated membrane glycoprotein
                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=89017240; PubMed=3174652;
Howe C.L., Granger B.L., Hull M., Green S.A., Gabel C.A., Helenius A.,
Mellman I.;
                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
05-JUL-2004 (Rel. 44, Last annotation update)
Lysosome-associated membrane glycoprotein 1 precursor (LAMP-1) (120
kDa lysosomal membrane glycoprotein) (LGP-120) (CD107A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       implicated in tumor cell metastasis.
--- SUBCELLULAR LOCATION: Type I membrane protein. Lysosomal. This protein shuttles between lysosomes, endosomes, and the plasma
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SEQUENCE OF 22-407 FROM N.A.
MEDLINE-89153580; PubMed-2920835;
Himeno M., Noguchi Y., Sasaki H., Tanaka Y., Furuno K., Kono A.
Sakaki Y., Kato K.;
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 283-357 FROM N.A. STRAIN=Wistar Kyoto; TISSUB=Aortic smooth muscle; STRAIN=Wistar Kyoto; TISSUB=Aortic smooth muscle; Adams L.A., Werny I., Schwartz S.M.; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                      Sakaki Y., Kato K.;
Isolation and sequencing of a cDNA clone encoding 107 kDa
sialoglycoprocein in rat liver lysosomal membranes.";
FBBS Lett. 244:351-356(1989).
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EMBL; X14765; CAA32833.1; -...
EMBL; U74766; AB19108.1; -...
PIR, A30200; A30200.
RGD; 2989; Lampl.
RGD; 2989; Lampl.
InterPro; IPR002500; Lamp.
Pfam; PF01299; Lamp.
PROSITE; PS00310; LAMP.
PROSITE; PS00311; LAMP.
PROSITE; PS00311; LAMP.
SIGNAL
SIGNAL
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                                            Name=Lamp1; Synonyms=Lamp-1;
Rattus norvegicus (Rat).
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"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-ATCC 49256;
Karpatral V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A., Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T., Haselkorn R., Overbeek R., Kyrpides N.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                 SERAIN=CSTBL/6; TISSUE=Lung;
MEDLINE=20530913; PubMed=11076861;
MEDLINE=20530913; PubMed=11076861;
MEDLINE=20530913; PubMed=11076861;
MEDLINE=20530913; PubMed=11076861;
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Naramatsu M., Inoue Y., Kira A., Haysahizaki Y.; sequencing pipeline with 384 multicapillary sequencer.",
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subsp. vincentii ATCC 49256.
Fusobacterales; Fusobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00336; LYSASSOCTDMP.
PROSITE; PS00310; LAMP_1; 2.
PROSITE; PS00311; LAMP_2; 1.
SEQUENCE 407 AA; 43936 MW; 696D0C79F627DA84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7P724;
01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
^1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2004 (TrEMBLrel. 26, Last se
01-MAR-2004 (TrEMBLrel. 26, Last an
Xaa-His dipeptidase (EC 3.4.13.3).
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Best Local Similarity 66....
6; Conservative
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Bacteria, Fusobacteria,
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281 GMNASSSLF 289
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STRANIE-SCABL/G17 IISSUE=Lung;
STRANIE-SCABL/G17 IISSUE=Lung;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last amoutoation update)
Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
clone:1200007101 product:lysosomal membrane glycoprotein 1, full
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MEDLINE=20499374; Pubmed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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25947490749A7C88 CRC64;
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MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.
High-efficiency full-length; CDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN-CSPL/60; TISSUE-Lung;
MEDINE-21085660; Pubmed-11217851;
RIKEN FANTOM CONSORTIUM;
                                                                                                                                                                                                                                                                                                                   SD
                                                                                                                                                                                                                                                                                                                                  43969 MW;
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les 6; Conservative
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281 GMNATSSLF 289
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293 2
329 3
359 3
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       Name=Lamp1;
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CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is DR GC GC:0016787; F:Metallopeptidase activity; IEA.
DR GO; GC:0008237; F:Metallopeptidase activity; IEA.
DR GO; GC:0008508; P:X-His dipeptidase activity; IEA.
DR GO; GC:0006508; P:X-His dipeptidase activity; IEA.
DR GO; GC:0006508; P:X-His dipeptidase activity; IEA.
DR GO; GC:0006508; P:X-His dipeptidase activity; IEA.
DR HIGETPO; IPRO1261; ArgE dapE.
DR InterPro; IPRO1261; ArgE dapE.
DR InterPro; IPRO1264; Peptidase_M20.
DR InterPro; IPRO1264; Peptidase_M20.
DR PETAMS; TIGRO1887; dipeptidase1ke; 1.
DR PROSTIE; PS00788; ARGE DAPE_CFG2_1; UNKNOWN_1.
KW Dipeptidase; Hydrolase.
SQ SEQUENCE 452 AA; 50268 MW; 8F64B0ACBE9406FA CRC64;
Accord Similarity 77.8%; Pred. No. 11.4-402;
Matches 7; CONServative 0; Mismatches 2; Indels 0; Gaps 0;
DD 260 GYNANSALF 268
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Search completed: October 26, 2004, 16:05:05 Job time : 42.6324 secs

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S. pheumo Streptoco

Klebsiell

S pneumon
M. tuberc
M. tuberc
Mycobacte
Human hea
Human lys
Human lys

Human lys Tumour ne Geniculos

Adk46701 Adm92204 Abm05204 Abb05887 Abb05887 Adj69797 Aadj69797 Aadj69797 Adm03755 Adm0375 Adm0

Haloperox

Drosophil

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This sequence represents a cyclic peptide derived from the Staphylococcus aucueus AgrD peptide. The invention relates to AgrD derived peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New cyclic peptides for treating infections with Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "N-terminal residue forms bond with C-terminal residue to form a cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus infection; cyclic peptide; AgrD; agr response; virulence factor; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     S. aureus peptide #6 used for bacterial interference.
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(UYNY ) UNIV NEW YORK STATE.
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Staphylococcus aureus.
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Misc-difference
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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MAYVILLE P.
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24-JUN-1999;
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                                                                                                                                                                                                                                                                  The present sequence is that of a novel synthetic cyclic peptide of the invention that is capable of inhibiting the agr response of staphylosoccus aureus. It is an AgrD-autoinducing peptide, where AgrD is secreted agr-encoded peptide and where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. Preferred peptides may have the sequence NH2-X(n)-2-X(y)-COM, with a cyclic bond between the Z residue and COCH other than a thioseter bond, where X is an amino acid, an amino acid analogue, a peptidomimetic or non-amide isostere, Z is a an amino acid analogue, a peptidomimetic or non-amide isostere, Z is a an amino acid analogue, a peptidomimetic or non-amide isostere, Z is a synthetic or a biosynthetic amino acid, act of and y is 1-10. The cyclic bond is especially a lactam or lactone bond. The thiololactone structure within native AgrD peptides is required for activation of the structure can destroy agr response activating activity while preserving and enhancing inhibitory activity. A claimed method of preparing a cyclic
                                                                                    ô
with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus \,
                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "note linked to residue 5 to form cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                            note= "note linked to residue 9 to form cyclic peptide"
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in a subject.
                                                                                                                                                                                                                                                                                         Staphylococcus aureus, AgrD; agr response, inhibitor; antibiotic; antibacterial; infection; therapy; cyclic.
                                                                                    0
                                                                                                                                                                                                                                                                   AgrD-autoinducing cyclic peptide, inhibitor of agr response.
                                                                                   Indels
                                                          94.9%; Score 37; DB 3; Length 9; 100.0%; Pred. No. 1.7e+06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                   note= "any amino acid"
                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novick RP,
                                                                                                                                                                                             AAM50905 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 7; Col 19; 18pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYRQ ) UNIV ROCKEFELLER.
(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                           (first entry)
                                                 Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mayville P,
                                                                                                                                  GVNAXSSAF 9
                                                                                                           1 GVNAXSSAF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-170774/22.
                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                      Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JAN-2002
                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                    AAM50905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muir TW,
                                                                                                                                                                      RESULT 2
                                                                                                                                                                                   AAM50905
  SXXX
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peptide involves: assembling a linear peptide chain on to a solid phase resin support; deprotecting the resulting protected assembled peptide; treating the deprotected peptide with neutral buffer for a time sufficient to form the cyclic peptide and cleave the peptide from the support; and recovering the cyclic peptide. The peptide is useful for bacterial interference, especially for the treatment of S. aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP51540 to ABP53547 represent cyclic peptides (I) from the present invention. The present invention also describes a method for treating Staphylococcus aureus infection comprising the administration of a composition comprising (I). (I) has antibacterial activity, and can be used as an agr gene response inhibitor. The peptides are useful for treating S. aureus infections
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyclic peptide; Staphylococcus aureus; infection; antibacterial; agr response inhibitor.
                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cyclic peptides, useful for treating Staphylococcus aureus
                                                                                                                                                                                                                                                       Score 37; DB 5; Length 9; Pred. No. 1.7e+06; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                          0; Indels
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1.7e+06;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "any amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
5'
                                                                                                                                                                                                                                          94.9%; Scor-
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novick RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP53546 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0090402P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                               9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                  1 GVNAXSSAF 9
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6

Matches

25-APR-2000

AAY67860;

AAY67860

g ò

WO9967286-A2

29-DEC-1999.

24-JUN-1999; 24-JUN-1998;

Muir TW,

Query Match

Best Loc Matches

ò g AAY67859;

MX S X B X B X B X B

RESULT 5 **AAY67859**

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This sequence represents the Staphylococcus aureus AgrDII derived composition. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus
                                                                                                                                                                                                                                                                                                                     New cyclic peptides for treating infections with Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Autoinducer-2; AI-2; antibiotic; antibacterial; dermatological; vulnerary; pheromone; agr system; accessory gene regulator; cyclic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                     Beavis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.6%; Score 33; DB 3; L
77.8%; Pred. No. 1.7e+06;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shokat K,
                                                                                                                                                                                                                                                     Ji G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schauder S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYPR-) UNIV PRINCETON.
(QUOR-) QUOREX PHARM INC.
(UYTE-) UNIV TECHNOLOGIES INT INC.
                                                                                                                                                                                                                                                     Novick RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB07160 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                      English
                                                                                                                                  99WO-US014562
                                                                                                                                                                  98US-00103438
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                                                                                                                                                                                                (UYRQ ) UNIV ROCKEFELLER.
(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 77.8
                                                                                                                                                                                                                                                                                                                                                      Example; Page 22; 37pp;
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                                                                                                                                                                                                                                                     Muir TW, Mayville P,
                                   Staphylococcus aureus.
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                                                                                                                                                                                                                                                                                   WPI; 2000-147202/13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GVNAASSLF
   virulence factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9 AA;
                                                                 WO9967286-A2
                                                                                                                                  24-JUN-1999;
                                                                                                                                                                  24-JUN-1998;
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07-DEC-2000;
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                                                                                                  29-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
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   Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the Staphylococcus aureus AgrDII derived peptide. The invention relates to AgrD derived cyclic peptides, a composition containing a peptide and a carriter, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New cyclic peptides for treating infections with Staphylococcus aureus
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                 Staphylococcus aureus infection; AgrD; agr response; treatment;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus infection; treatment; AgrD; agr response;
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0
 Indels
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Pred. No. 1.7e+06;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                Staphylococcus aureus AgrDII derived peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus AgrDII derived peptide sequence.
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Mismatches
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                                                                                                                                               AAY67860 standard; peptide; 9 AA.
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(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                (first entry)
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mayville P,
                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus
                               σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-147202/13.
                               GVNAXSSAF
                                                            GVNAXSSAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GVNAXSSAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                   virulence factor.
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24-JUN-1998;
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               Muir TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                        subject.
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8
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                                                                                                                                                                         The invention relates to the use of autoinducer-2 (AI-2) agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating becterial growth and pathogenesis. Synezyistic antibiotic compositions comprising inhibitors of the quorum-sensing pathway of a microorganism are also provided. Methods using such AI-2 analogues are useful for treating pathogen-associated disease states. The compounds and antibiotic compositions can be used to inhibit bacterial cell growth and/or biofilm formation on a medical device, particularly for promoting growth of skin graft replacements used in the treatment of burns and ulcers. They may also be used to aid wound repair, and to inhibit bacterial cell growth and biofilm formation in or on products or devices used for personal hygiene. The present sequence represents a inhibitor of peptide-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "note linked to residue 9 to form cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "note linked to residue 5 to form cyclic peptide"
                                                         Use of autoinducer-2 agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis, also antibiotic compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic; antibacterial; infection; therapy; cyclic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.6%; Score 33; DB 5; Length 9; 77.8%; Pred. No. 1.7e+06; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protected peptide used in cyclic peptide production.
                                                                                                                                             Disclosure; Page 33; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "Ser(tBu)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Ser(Bzl)"
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(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GVNAXSSAF 9
                   WPI; 2002-075235/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVNASSSLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                         quorum sensing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9 AA;
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Modified-site
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ID AAMSO 80007

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the preparation of novel synthetic cyclic peptides of the invention (see AAM50899-906). The peptide corresponds to the Staphylococcus aureus agric on a Wang-resin using an Fmoc N-alpha protection strategy. Following chain assembly, the peptide was cleaved from the support and the Ser-5 residue deprotected by treatment with a trifluoroaccial protected codianisols:water mixture (90:55) for 4 hr. The partially protected peptide anaboxylates were then dissolved in DMF and treated with PyBOPs and a catallytic amount of dimethylaminopyridine. Cycliation was complete after 2 hr. The remaining protecting groups were then removed by treatment with HP and the peptide by HPLC. The cyclic peptide is capable of inhibiting the agr response of Staphylococcus aureus. The thioloaccone structure within native AgrD peptides is required for activation of this response. Replacement of the thiol ester component of the cyclic ring structure with a lactone (as in the present case) or a lactam can destroy agr response activating activity while preserving and enhancing inhibitory activity. The cyclic peptides are useful for bacterial interference, especially for the treatment of S. aureus
                                                                                                                                                                                                                                                                                                                                          sequence is that of a protected peptide used in an example of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "note linked to residue 9 to form cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "note linked to residue 5 to form cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AgrD2, agr response; inhibitor; antibiotic; antibacterial; infection; therapy; lactone; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                               Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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   Beavis
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Novick RP,
                                                                                                                                                                                                                                                                         Disclosure; Col 14; 18pp; English.
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(first entry)
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Synthetic.
   Mayville P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ഗ
                                                                 WPI; 2002-170774/22
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08-MAY-2002
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The present sequence is that of a novel synthetic AgrD2 lactone cyclic peptide in which residue 5 of the peptide is linked to residue 9 via a lactone bond. The peptide is lactone bond. The peptide is derived from an AgrD2 peptide 9 via a strone bond. The peptide is derived from an AgrD2 peptide of factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthesis of virulence factor and other carracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agric protein activity of the support of the inhibition of the agr response to be monitored spectrophotometrically. The lactone AgrD2 peptide inhibited the agr response of group I S. aureus strains without activating them agr response of group I S. aureus strains without provides claimed cyclic peptides (see AAMS0899-906 and AAMS0899) and methods for preparing them, especially peptides where the cyclic bond is a lactone bond. The cyclic peptides are useful for bacterial interference, septically for the treatment of S. aureus infection.
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                                                                                                                                    Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in a subject.
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84.6%; Score 33; DB 5; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 2; Indels
                                                                     Beavis
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                                                                 Mayville P, Novick RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM51003 standard; peptide; 9 AA.
                                                                                                                                                                                                         Example 1; Col 9; 18pp; English.
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             (UYRQ ) UNIV ROCKEFELLER.
(UYNY ) UNIV NEW YORK STATE.
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(UYNY ) UNIV NEW YORK STATE.
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9 AA;
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                                                                 Muir TW,
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The present sequence is that of a novel synthetic AgrD2 linear free acid peptide. The peptide is derived from the cyclic AgrD2 peptide of Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agr3 promoter. This allowed activation or inhibition of the agr response to be monitored spectrophotometrically. Unlike an Agr2 thiololactone cyclic peptide (see AAMS1001), the present peptide was unable to either activate or inhibit the agr response, even when added to cultured cells at un concentrations. The invention provides claimed cyclic peptides and AAMS09999 and methods for preparing them. The cyclic peptides are useful for bacterial interference, especially for the treatment of S. aureus infection
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in a subject.
             Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in
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                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 5; Length 9;
Pred..No. 1.7e+06;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM51002 standard; peptide; 9 AA.
                                                                       English.
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                                                                                                                                                                                                                                                                                                                                                                                   84.68;
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(UYNY ) UNIV NEW YORK STATE.
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                      Example 1; Col 9; 18pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus.
Synthetic.
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Modified-site
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                                            subject.
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Gaps

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Length 9;

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activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus
                                                                                          82.1%;
88.9%;
                                                                                                                        Conservative
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Best Local Similarity
Matches 8; Conserv
                                                                                                        Similarity
8; Conserv
                                                                                                                                                     1 GVNAXSSAF
                                                                                                                                                                                GVNAXSSLF
                                                                                                                                                                                                                                                                                                                                                                                               virulence factor.
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                                                             Sequence 9 AA;
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Matches
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                              The present sequence is that of a novel synthetic AgrD2 linear thioester peptide. The peptide is derived from the cyclic AgrD2 linear thioester Staphylococcus aureus group II. AgrD2 is a secreted agr-encoded peptide, where the agr locus controls the synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agr3 promoter. This allowed activation or inhibition of the agr response to be monitored spectrophotometrically. Unlike an AgrD2 thiololactone cyclic peptide (see AAMS1001), the present peptide was unable to atther activate or inhibit the agr response, even when added to cultured cells at um concentrations. The invention provides claimed cyclic peptides (see AAMS10999) and methods for preparing them. The cyclic peptides (see AAMS10999) and methods for preparing them. The cyclic peptides (see AAMS1089-906 and AAMS1099) in therference, especially for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a cyclic peptide derived from the Staphylococcus aureus AgrD peptide. The invention relates to AgrD derived peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New cyclic peptides for treating infections with Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus infection; cyclic peptide; AgrD; agr response;
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                                                                                                                                                                                                                                                                                                     84.6%; Score 33; DB 5; Length 9; 77.8%; Pred. No. 1.7e+06; Live 0; Mismatches 2; Indels

    S. aureus peptide #1 used for bacterial interference.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY67851 standard; peptide; 9 AA
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      Example 1; Col 9; 18pp; English
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(UYNY ) UNIV NEW YORK STATE.
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Best Local Similarity 7...
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                               GVNAASSLF
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Misc-difference
                                                                                                                                                                                                                                                                            Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY67851;
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AAY67851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New cyclic peptides for treating infections with Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus infection; AgrD; agr response; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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88.9%; Pred. No. 1.7e+06;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus AgrDII derived peptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
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Score 32; DB 3; I
Pred. No. 1.7e+06;
); Mismatches 1;
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                                                                                                                                                                                                                                                                                                             AAY67861 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Page 22; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US014562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-00103438,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYRQ ) UNIV ROCKEFELLER.
(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muir TW, Mayville P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus
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/note= "note linked to residue 9 to form cyclic peptide"

Location/Qualifiers

Misc-difference Misc-difference Misc-difference

Staphylococcus aureus

Synthetic.

AgrD2, agr response; inhibitor; antibiotic; antibacterial; infection; therapy; cyclic.

AgrD2 lactam cyclic peptide.

(revised)
(first entry)

07-AUG-2003 08-MAY-2002

/note= "note linked to residue 5 to form cyclic peptide"

'note= "any amino acid"

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The invention relates to the use of autoinducer-2 (AI-2) agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis. Synergistic antibiotic compositions comprising inhibitors of the quorum-sensing pathway of a microorganism are also provided. Methods using such AI-2 analogues are useful for treating pathogen-associated disease states. The compounds and antibiotic compositions can be used to inhibit bacterial cell growth and/or biofilm formation on a medical device, particularly for promoting growth of skin graft replacements used in the treatment of burns and ulcers. They may also be used to aid wound repair, and to inhibit bacterial cell growth and biofilm formation in or on products or devices used for personal hygiene. The present sequence represents a inhibitor of peptide-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of autoinducer-2 agonists or antagonists for regulating activity of autoinducer-2 receptor, regulating bacterial growth and pathogenesis, also antibiotic compositions.
                                                                                                                                    Autoinducer-2; AI-2; antibiotic; antibacterial; dermatological;
vulnerary; pheromone; agr system; accessory gene regulator; cyclic.
                                                                                                     Peptide-mediated quorum sensing inhibitor peptide cyclo-XIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stein J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 5; Length 9;
Pred. No. 1.7e+06;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                           'note= "diaminoprprionic acid residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shokat K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schauder S,
                                                                                                                                                                                                                Location/Qualifiers
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 33; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYPR-) UNIV PRINCETON.
(QUOR-) QUOREX PHARM INC.
(UYTE-) UNIV TECHNOLOGIES INT INC.
ABB07161 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                               10-MAY-2001; 2001WO-US015221
                                                                                                                                                                                                                                                                                                                                                                                             10-MAY-2000; 2000US-0203000P.
07-DEC-2000; 2000US-0254398P.
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88.9%;
                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dammel CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-075235/10.
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                          WO200185664-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quorum sensing
                                                                                                                                                                                                                         Key
Modified-site
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                                                                    13-MAR-2002
                                                                                                                                                                                                                                                                                                                            15-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bassler BL,
                                                                                                                                                                                        Synthetic.
                                  ABB07161;
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Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in a

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Beavis R,

Novick RP,

Muir TW, Mayville P,

WPI; 2002-170774/22.

(UYRQ) UNIV ROCKEFELLER. (UYNY) UNIV NEW YORK STATE.

99US-00339511 98US-0090402P

24-JUN-1999; 24-JUN-1998;

US6337385-B1

08-JAN-2002.

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The present sequence is that of a novel synthetic AgrD2 lactam cyclic peptide in which residue 5 of the peptide is linked to residue 9 via a lactam bond. The peptide is derived from an AgrD2 peptide 9 via a strand bond. The peptide is derived from an AgrD2 peptide 9 via a strand bond. The peptide is derived from an AgrD2 peptide 9 via a strand bond. The synthesis of virulence factor and other extracellular proteins responsible for pathogenicity in S. aureus. The biological activity of the synthetic peptide was assayed using cultured S. aureus strains containing a beta-lactamase reporter gene fused to the agrical peptide approacher. This allowed activation or inhibition of the agr response in group I S. aureus strains and did not continue the agr response in group I S. aureus strains and did not cotinue the agr response in group I S. aureus strains and did not cotinue the agr response in group I S. aureus strains and did not methods for preparing them, especially where the cyclic bond is a lactam cortone bond. The cyclic peptides (see AAMS0899-906 and AAMS0899-106 and nethods for preparing them, especially where the cyclic bond is a lactam interference, especially for the treatment of S. aureus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·;
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0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32; DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Col 11; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM50908 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9 AA;
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ID AAM5
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Gaps

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8; Conservative

1 GVNAXSSAF GVNAXSSLF

ò 유 AAM51005 standard; peptide; 9 AA.

RESULT 14 AAM51005 AAM51005;

SXB

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The present sequence is that of a protected peptide used in an example of the preparation of novel synthetic cyclic peptides of the invention (see AAMS0899-960. The peptide corresponds to the Staphylococcus aureus AAMS089-960. The peptide corresponds to the Staphylococcus aureus carbon a grant sequence with a Cyss to diaminopropionic acid (Dpr) mutation (lactam). It was synthesised on a Wang-resin using an Fmoc N-alpha protection strategy. Following chain assembly, the peptide was cleaved from the support and the Dpr-5 residue deprotected by treatment with a trifluoroacetic acid:anisole:water mixture (90:5:5) for 4 hr. The partially protecting groups were removed by treatment with HF and the peptide purified by HPLC. The cyclic peptide is capable of inhibiting the captide purified by HPLC. The cyclic peptide is capable of inhibiting the peptide purified by HPLC. The cyclic peptide is capable of inhibiting the captive AgrD peptides is required for activation of this response. Replacement of the thiol ester component of the cyclic ring structure within a lactam (as in the present case) or a lactone can destroy agr cresponse activating activity while preserving and enhancing inhibitory activity. The cyclic peptides are useful for bacterial interference,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Col 14; 18pp; English.
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Gaps

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82.1%; Score 32; DB 5; Length 9; 88.9%; Pred. No. 1.7e+06; tive 0; Mismatches 1; Indels

Query Match
Best Local Similarity 88.9
Matches 8; Conservative

Sequence 9 AA;

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note= "note linked to residue 9 to form cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "note linked to residue 5 to form cyclic peptide"
                                                                                                              Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic; antibacterial; infection; therapy; cyclic.
                                                                          Protected peptide used in cyclic peptide production.
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                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novick RP,
                                                                                                                                                                                                                                                                                                                                                                          note= "Ser(Bzl)"
                                                                                                                                                                                                                                                                                                                                                                                                               note= "Ser(Bzl)"
                                                                                                                                                                                                                                                                                                                                  /label= Dpr(Boc)
                                                                                                                                                                                                                                                     note= "Z-Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0090402P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-00339511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYRQ ) UNIV ROCKEFELLER.
(UYNY ) UNIV NEW YORK STATE.
                                     08-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muir TW, Mayville P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-170774/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                          Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-JUN-1999;
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                                                                                                                                                                          Synthetic.
AAM50908;
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1 GVNAXSSLF
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GVNAXSSAF

Search completed: October 26, 2004, 15:59:46 Job time : 43.75 secs

Sequence 26, Appl Sequence 26, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 5, Appli Sequence 6, Appli Sequence 105919, Sequence 105919, Sequence 15919, Sequence 15919, Sequence 594, Appl Sequence 694, Appl Sequence 694, Appl Sequence 694, Appl Sequence 695, Appl

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US-10-32-950-7

(Sequence 7, Application US/10032950

(Sequence 7) Application No. US20020077453A1

(Sequence 7) Application No. US20020077453A1

(SENEMAL INFORMATION:

(APPLICANT: Mayville, Patricia

(APPLICANT: Mayville, Patricia

(APPLICANT: Beavis, Ronald

(APPLICANT: Beavis, Ronald

(APPLICANT: Beavis, Ronald

(APPLICANT: US-100200077453A1ick, Richard P.

(APPLICANT: US-100200077453A1ick, Richard P.

(AUGAGYON)

(AUGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 94.9%; Score 37; DB 13; Length 9; Best Local Similarity 100.0%; Pred. No. 1.2e+06; Matches 9; Conservative 0; Mismatches 0; Indels
             4 US-10-371-525-26

4 US-10-371-669-26

4 US-10-371-669-26

4 US-10-371-260-26

4 US-10-371-260-26

4 US-10-371-260-26

4 US-10-371-260-26

4 US-10-371-260-26

4 US-10-151-557-2

8 US-10-151-557-2

8 US-10-151-557-2

8 US-10-424-599-214693

8 US-10-437-963-105919

8 US-10-437-963-105919

8 US-10-437-963-105919

8 US-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-10-78-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                    1 GVNAXSSAF 9
TYPE: PRT
à
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Sequence 260065,
Sequence 3, Appli
Sequence 3, Appli
Sequence 181018,
Sequence 181018,
Sequence 155, App
Sequence 155, App
Sequence 155, App
Sequence 538, App
Sequence 538, App
Sequence 538, App
Sequence 538, App
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                                                                                                                                        October 26, 2004, 15:54:00 ; Search time 31.5 Seconds (without alignments) 92.502 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-032-950-1
US-10-0201-444-3
US-10-201-444-6
US-10-201-444-6
US-10-201-444-6
US-10-424-599-1272038
US-10-080-170-155
US-10-080-170-155
US-10-080-170-155
US-10-080-170-155
US-10-080-170-155
US-10-080-170-538
US-10-080-170-538
US-10-080-170-538
US-10-080-170-538
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Maximum Match 100%
Listing first 45 summaries
                                                                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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39
1 GVNAXSSAF 9
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Match Length
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No.
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59731, A 59936, A 182847,

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Gaps

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Sequence 181018, Application US/10424599; Publication No. US20040031072A1; Publication No. US20040031072A1; Publication No. US20040031072A1; Publication No. US20040031072A1; APPLICANT: La Rosa Thomas J. APPLICANT: APPLICANT: Zhou Yihua APPLICANT: Zhou Yihua APPLICANT: Cao Yongwei TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement; FILE REFERENCE: 38-21(53223)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-201-444-6

| Sequence 6, Application US/10201444
| Sequence 6, Application US/10201444
| Publication No. US20030078378A1
| GENERAL INFORMATION:
| APPLICANT: New York University Medical Center
| TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
| TITLE OF INVENTION NUMBER: US/10/201,444
| CURRENT FILING DATE: 1997-05-23
| PRIOR APPLICATION NUMBER: US/08/861,476
| PRIOR FILING DATE: 1997-05-22
| NUMBER OF SEQ ID NOS: 8
| SOFTWARE: Patentin version 3.0
| SEQ ID NO 6
                                                                                                      Sequence 3, Application US/10201444

Sequence 3, Application US/10201444

GENERAL INFORMATION:
Publication No. US20030078378A1

GENERAL INFORMATION:
FILE REFERENCE: 63753/7

CURRENT FILING DATE: 105/10/201,444

CURRENT FILING DATE: 105/10/201,444

FILE REFERENCE: 63753/7

CURRENT FILING DATE: 197-05-22

PRIOR FILING DATE: 197-05-22

SOFTWARE: Patentin version 3.0

SOFTWARE: Patentin version 3.0

SOFTWARE: Patentin version 3.0
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Pred. No. 12;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-201-444-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-201-444-6
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Best Local Similarity 77.8%;
Matches 7; Conservative (
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Best Local Similarity
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APPLICANT: La Rosa Thomas J
APPLICANT: En Rosa Thomas J
APPLICANT: About K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 260065
LENGTH: 112
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                                                                                                                                           Sequence 1, Application US/10032950;
Publication No. US20020077453A1
General INPORMATION:
GENERAL INPORMATION:
APPLICANT: Mulr, Tom
APPLICANT: Mayville, Patricia
APPLICANT: No. US20020077453A1ick, Richard P.
APPLICANT: No. US20020077453A1ick, Richard P.
APPLICANT: Ji, Guangyond
APPLICANT: Ji, Guangyond
TITLE OF INVENTION: INTERFERENCE
TITLE OF INVENTION: INTERFERENCE
TITLE OF INVENTION: INTERFERENCE
TITLE OF INVENTION: UNMER: US/10/032,950
CURRENT APPLICATION NUMBER: US/10/032,950
CURRENT APPLICATION NUMBER: 60/990,402
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Peptide NAME/KEY: VARIANT COTHER INFORMATION: (5) OTHER INFORMATION: (5) OTHER INFORMATION: Xaa represents any amino acid at this position. US-10-032-950-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
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82.1%; Score 32; DB 15; Length 112;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.1%; Score 32; DB 13; Length 9; 88.9%; Pred. No. 1.2e+06; Live 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 260065, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 88.9
Matches 8; Conservative
1 GVNAXSSAF 9
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ORGANISM: Glycine max
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Sequence 155, Application US/10468356
; Sequence 155, Application US/10468356
; Bublication No. US20040197896A1
; GENERAL INFORMATION:
    APPLICANT: COLE, STEWART
    TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENEOMICS AS A TOOL FOR
    TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
; TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
; FILE REFERENCE: 05394.001
; CURRENT APPLICATION NUMBER: US/10/468,356
CURRENT FILING DATE: 2003-08-19
; PRIOR FILING DATE: 2003-02-22
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 655
; SOFTWARE: PALENTIN Ver. 3.2
; SEQ ID NO 155

                                                                                                                                                                                                                                                                                                                                                           Publication No. US20040121322A9
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR FILE REFERENCE: 03495,0218
FILE REFERENCE: 03495,0218
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.9%; Score 30; DB 16; Length 163; 77.8%; Pred. No. 79;
                                                                                                              Length 163;
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                                                                                                         Query Match
Rest Local Similarity 77.8%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 2;
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ORGANISM: Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Mycobacterium leprae
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-10-080-170-155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 77.8
Matches 7; Conservative
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US-10-468-356-155
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APPLICANT: La Rosa Thomas J
APPLICANT: Execution David K
APPLICANT: And Vibra
APPLICANT: And Vibra
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
SEO ID NO 572035
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TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
FILE REFERENCE: 03495.0218
CURRENT APPLICATION NUMBER: US/10/080,170
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
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                                                                                                                                                                                                                                                           Length 54;
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                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_87667C.1.pep
US-10-424-599-272035
                                                                                                                                                                                                                                                        Score 31; DB 15;
Pred. No. 14;
0; Mismatches 1
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OTHER INFORMATION: unsure at all Xaa locations
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CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 181018
LENGTH: 54
TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 272035, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 155, Application US/10080170 Publication No. US20030129601A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
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Best Local Similarity 66.,
6, Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 155
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TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENEOMICS AS A TOOL FOR TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES FILE REFERENCE: 05394.019

CURRENT APPLICATION NUMBER: US/10/468,356

CURRENT FILING DATE: 2003-08-19

PRIOR FILING DATE: 2003-08-19

PRIOR FILING DATE: 2002-02-2

PRIOR FILING DATE: 2002-02-2

PRIOR FILING DATE: 2002-02-2

SOFTWARE: PLANG DATE: 2002-22

SOFTWARE: PLANG DATE: 2003-08-19

NUMBER OF SEQ ID NOS: 655

SEQ ID NO 538

LENGTH: 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1603, Application US/10408765A; Bequence 1603, Application US/10408765A; Publication No. US20040101874A1; GENERAL INFORMATION: SCOUNTING SOUNTING STEVEN W. APPLICANT: Taylor, Steven W. APPLICANT: Warnork, Dale E. TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION TITLE OF INVENTION: TARGETS FOR THE BRITOCHONDRIAL PROFEOME FILE REPRENCE: 660088.465; CURRENT APPLICATION NUMBER: US/10/408,765A; CURRENT FILING DATE: 2003-04-04.

NUMBER OF ERQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1603
LENGTH: 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 30, DB 17; Length 167; Pred. No. 81; 2; Indels 0; Mismatches 2; Indels
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Pred. No. 1.6e+02;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-468-356-538
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 66.7%;
Matches 6; Conservative
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CORGANISM: Homo sapiens
US-10-408-765A-1603
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US-10-408-765A-1603
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US-10-371-525-26
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                                                                                                                                                                             Sequence 538, Application US/10080170
| Publication No. US20030129601A1
| GENERAL INFORMATION |
| TITLE OF INVENTION: COLE, S.T. |
| TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR |
| TITLE OF INVENTION: COMPARATIVE MYCOBACTERIOSES |
| TITLE OF INVENTION: COMPARATIVE MYCOBACTERIOSES |
| TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES |
| TITLE OF INVENTION: 1010 |
| TITLE OF INVENTION: 1020 |
| TITLE OF INVENTION WHERER: US/10/080,170 |
| CURRENT FILING DATE: 2001-02-22 |
| NUMBER OF SEQ ID NOS: 652 |
| SOFTWARE: Patentin Ver. 2.1 |
| LENGTH: 167
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Fublication No. US20040121322A9

Fublication No. US2004012132A9

Fublication No. US2004012132A9

Fublication No. US2004012132A9

FILE INCRMATION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR

TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR

TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR

TITLE OF INVENTION: 10ENTERS. US/10/080,170

CURRENT APPLICATION NUMBER: US/10/080,170

FRICE APPLICATION NUMBER: 60/270,123

PRIOR FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 652

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 538
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Pred. No. 81;
0; Mismatches 2; Indels
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CRGANISM: Mycobacterium tuberculosis
US-10-080-170-538
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, ORGANISM: Mycobacterium tuberculosis
US-10-080-170-538
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US-10-468-356-538
US-10-468-356-538
Publication US/10468356
Publication No. US20040197895A1
GENERAL INFORMATION:
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
                                              132 GVAAASSAF 140
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     1 GVNAXSSAF 9
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                                                                                                                                    RESULT 11
US-10-080-170-538
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US-10-080-170-538
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Livingston, Brian Chesnut, Robert W. Epimmune Inc.

APPLICANT: APPLICANT:

APPLICANT: COLE, STEWART

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Gaps

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; TITLE OF INVENTION: Expression Vectors for Stimulating an FITLE OF INVENTION: Immune Response and Methods of Using the Same; FILE REPREBRICE: 3963-20022.01; CURRENT APPLICATION NUMBER: US/10/371,525 CURRENT FILING DATE: 2003-02-21; PRIOR APPLICATION NUMBER: US 60/085,751; NUMBER: OF SEQ ID NOS: 463; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 26; LENGTH: 416; TYPE: PRI CORPALISM: Homo sapiens; FEATURE: HOmo sapiens; FEATURE: US-07HER INFORMATION: human lysosomal membrane glycoprotein-1 (LAMP-1); US-10-371-525-26
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Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels
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290 GMNASSSRF 298
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 26, 2004, 15:46:55; search time 8.73529 Seconds (without alignments) 99.132 Million cell updates/sec Run on:

US-10-032-950-7 39 1 GVNAXSSAF 9 Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	AgrD protein [impo	ical r	hypothetical prote	d hyp	hypothetical prote	hypothetical prote	7	P2B/LAMP-1 precurs	120K lysosomal mem	lysosome-associate	zip protein precur	hypothetical prote	urease accessory p	tion p	connexin 31 - huma	connexin 31 - mous	gap junction prote	ap junction	ylornith	ferrichrome ABC tr	•	hypothetical prote	hypothetical prote	gene 112 protein -	laminin alpha 5 ch	conserved hypothet	hypothetical prote	phage minor tail p	yigw protein - Esc
SUMMAKIES	ID	C89995	B95192	86	A87066	C70866	T45243	A28067	A60534	A30200	A31959	EPFF	T23740	T50707	A38737	JE0274	S23590	B43433	D42053	B69315	C69812	875327	AD3037	G98248	T03319		A82434	\$50624	AC3420	m
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probable deoxyribo	cytoplasmic Dnase	hypothetical prote	oxidoreductase yrb	hypothetical prote	probable iron-side	COSBS.3 protein (c	hypothetical prote	protein C05B5.3 [i	tubulin beta chain	probable DNA-bindi	mocR protein - Rhi	nerve growth facto	probable plcA prot	hypothetical prote	auxin-resistance p
AF0915	A91225	G86071	E86832	T04754	AC0187	843574	F85056	C88571	\$18597	G96713	851574	A32225	H70662	G86349	835071
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260	260	264	326	332	346	364	398	401	453	486	493	508	512,	523	540
71.8	71.8	71.8	71.8	71.8	71.8	71.8	71.8	71.8	71.8	71.8	71.8	71.8	71.8	71.8	71.8
28	28	28	28	28	28	28	28	58	28	28	28	28	58	28	28
30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 (28995) AgrD protein [imported] - Staphylococcus aureus (strain N315) (5)Species: Staphylococcus aureus (5)Species: Staphylococcus aureus (5)Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004 (5)Accession: (89995) (7)Accession: (89995) (8)Kuroda, M., Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.	A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUD:21311952; PMID:11418146 A;Accession: C89995 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-47 < KUR> A;Cross-references: UNIPROT:033586; GB:BA000018; PID:g13701831; PIDN:BAB43124.1; GSPDB:A;Experimental source: strain N315 C;Genetics: A;Gene: agrD	Query Match Best Local Similarity 77.8%; Pred. No. 2; Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Qy 1 GVNAXSSAF 9
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RESULT 2

24 GVNACSSLF 32

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hypothetical protein SP1652 (imported] - Streptococcus pneumoniae (strain TIGR4)
C;Date: Streptococcus pneumoniae
C;Date: O3-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: B95192
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heison, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Accession: B95192
A;Stetus: preliminary
A;Reference number: Ap5000; MUID:21357209; PMID:11463916
A;Accession: B95192
A;Stetus: preliminary
A;Residues: 1-924 «AUR»
A;Cross-references: UNIPROT:097PG8; GB:AE005672; PIDN:AAK75731.1; PID:g14973142; GSPDB:: C;Genetics:
A;Genetics:
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(Species: Mus musculus (house mouse)
(Species: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
(Shacession: A28067
(Sha
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C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
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R;James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, March 1999
A;Reference number: 222949
A;Reference number: 222949
A;Reference number: 222949
A;Reference number: 222949
A;Recession: T42243
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-169 cJAM-
A;Residues: 1-169 cJAM-
A;Cross-references: UNIPROT:Q9X7B5; EMBL:AL049913; PIDN:CAB43162.1
A;Experimental source: cosmid B1610
C;Genetics:
A;Note: MLCB1610.16
C;Superfamily: Mycobacterium leprae hypothetical protein MLCB1610.16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: Rv2468c
C;Superfamily: Mycobacterium leprae hypothetical protein MLCB1610.16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 167;
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Pred. No. 13;
0; Mismatches
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Matches 7; Conservative
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Best Local Similarity
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A87066

conserved hypothetical protein ML1255 [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: A87066
R;Cole, S.T.; Biglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hc
R; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, eam, M.A.; Rutter, S.; Seeger, K.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Authors: A86909; MUID:21128732; PMID:11234002
A;Accession: A87066
A;Scatus: preliminary
A;Molecule type: DNA
A;Residues: 1-163 <STO>
A;Cross-references: UNIPROT:Q9CC58; GB:AL450380; NID:g13093193; PIDN:CAC31636.1; GSPDB:G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cybecies Streptococcus pneumoniae (strain R6)
C; Species: Streptococcus pneumoniae (strain R6)
C; Species: Streptococcus pneumoniae
C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C; Accession: G98058
R; Accession: G98058
R; Hoskins, J.A.; Alborn Jr., W; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E. R; Hoskins, J.A.; Alborn Jr., W; Arnold, J.; Blaszczak, L.; Burgett, S.; McAhren, S.; M. Y. P.; Sun, P.M.; Vong-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; Jattle: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A; Reference number: A97872; MUID:21429245; PMID:11544234
A; Accession: G98058
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-924 < KUR>
A; Residues: 1-924 < KUR>
A; Genetics:
A; Genetics:
A; Genetics:
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C;Superfamily: Mycobacterium leprae hypothetical protein MLCB1610.16
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79.5%; Score 31; DB 2; Length 924; 66.7%; Pred. No. 47; ive 2; Mismatches 1; Indels
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Pred. No. 47;
2; Mismatches 1; Indels
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Pred. No. 13;
0; Mismatches 2; Indels
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Best Local Similarity 77.8%;
Matches 7; Conservative
                                                  Local Similarity 66.7
Les 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local S.
Matches 6
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hypothetical protein Rv2468c - Mycobacterium tuberculosis (strain H37RV)

RESULT 5

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C;Genetics:

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GMNATSSLF

281

C; Keywords: glycoprotein; membrane protein

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A, Residue Lype: DAMA
A, Residues: 1-416 < csAM>
A, Note: sequence extracted from NCBI backbone (NCBIP:129878)
A, Note: sequence extracted from NCBI backbone (NCBIP:129878)
A, Note: sequence extracted from NCBI backbone (NCBIP:129878)
A, Title: Purification and characterization of human lysosomal membrane glycoproteins.
A, Reference mumber: S02150; MUID:89104438; PMID:2912382
A, Recession: S02150
A, Rolecule type: protein
A, Residues: 28-35, X', 37-39, X', 41-43, X', 45-58 < MAN>
B, Residues: 28-35, X', 37-39, X', 41-43, X', 45-58 < MAN>
A, Title: The polylactosaminoglycans of human lysosomal membrane glycoproteins lamp-1 an A, Reference number: A265, A26556
A, Accession: A26556
A, A2656
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-416 <FUKA
A;Cross.references: UNIPROT:P11279; GB:J04182; NID:g186927; PIDN:AAA60382.1; PID:g30710:
R;Sawada, R:; Jardine, K.A.; Fukuda, M.
B:Gol. Chem. 268, 9014-9022, 1993
A;Title: The genes of major lysosomal membrane glycoproteins, lamp-1 and lamp-2. 5'-flan
A;Reference number: A46044; MUID:93232065; PMID:8517882
                                                                                                                                                                              1ysosome-associated membrane protein 1 precursor - human NiAlternate names: lysosomal-associated membrane protein lamp A; major lysosomal membrane; Species Homo sapiens (man) (Species Homo sapiens (man) (C)Species Homo sapiens (man) (C)Date: 31-Mar-1990 #sequence revision 01-Dec-1995 #text change 09-Jul-2004 (C)Accession: A31959; B46044; $02150; A23656; A32685; S34737; A30210; B30210 (C)Accession: A31959; B46044; $02150; A23656; A32685; S34737; A30210; B30210 (C)Accession: A31959; B46044; B4044; B4044
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Jymoleoule type: protein

Jymoleoule type: protein
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Modecule type: protein
A;Residues: 190-214 <CA3>
R;Viitala, J.; Carlsson, S.R.; Siebert, P.D.; Fukuda, M.
R;Viitala, J.; Carlsson, S.R.; 31347, 1988
A;Viitala, Molecular Sol. W.S.A. 85, 3743-3747, 1988
A;Title: Molecular cloning of cDNAs encoding lamp A, a human lysosomal membrane glycopring A;Reference number: A30210; WUID:88234502; PMID:3131762
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,Residues: 116-119,'X',121-128,'X',130-131,'X',133-135;163,'X',165-179,'X',181-189,'X'
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A;Molecule type: protein
A;Rolecule type: protein
B;Rolecule type: protein
B;Carlsson, S.R.; Fukuda, M.
J. Bhlol. Chem. 264, 20526-20531, 1989
J. Bhlol. Chem. 264, 20526-20531, 1989
A;Title: Structure of human lysosomal membrane glycoprotein 1. Assignment of A;Reference number: A32685; MUID:90062189; PMID:2584229
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A;Cross-references: GB:J03263; NID:g187178; PIDN:AAA59524.1; PID:g307132
A;Accession: B30210
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A;Status: preliminary; nucleic acid sequence not shown; not
A;Molecule type: DNA
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A;Map position: 13g34-13g34
C;Superfamily: lysosome-associated membrane protein
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C,Date: 17-Apr.1993 #sequence_revision 17-Apr.1993 #text_change 09-Jul-2004
C,Accession: A60534
R,Heffernan, M.; Yousefit, S.; Dennis, J.W.
Cancer Res. 49, 6077-6084, 1989
A;Title: Molecular characterization of P2B/LAMP-1, a major protein target of a metastasi A,Accession: A60534; MUID:90002989; PMID:2676155
A,Accession: A60534
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A; Residues: 1-407 <HONA
A; Cross-references: UNIPROT:P14562; EMBL:J03672
A; Note: the authors translated the codon GGG for residue 15 as Val
F; Minmen, M.; Noguchi, Y.; Sasaki, H.; Tanaka, Y.; Furuno, K.; Kono, A.; Sakaki, Y.; Kat
FEBS Lett. 244, 351-356, 1989
A; Title: Isolation and sequencing of a cDNA clone encoding 107 kDa sialoglycoprotein in
A; Reference number: S03331; MUID:89153580; PMID:2920835
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A, Residues: 22-407 <hIM>
A, Residues: 22-407 <hIM>
A, Cross-references: EMBL:X14765, NID:956577; PIDN:CAA32873.1; PID:956578
A, Note: part of this sequence, including the amino end of the mature protein, was confir
C, Superfamily: 1 yeosome-associated membrane protein
C; Keywords: glycoprotein; membrane protein
F; 22-407/Product: lysosomal membrane glycoprotein, 107K #status experimental <MAT>
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-0ct-1989 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
                                                                                                                                  Gaps
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            Length 382;
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A;Residues: 1-405 <HEF>
A;Cross-references: UNIPROT:P11438
C;Superfamily: lysosome-associated membrane protein
            DB 2;
32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 30; DB 2;
Pred. No. 34;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 30; DB 2;
Pred. No. 34;
1; Mismatches
                                                                                                                            Mismatches
            Score 30;
Pred. No.
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      76.9%;
66.7%;
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Best Local Similarity 66...
                                                                                                                            Conservative
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256 GMNASSSLF 264
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                                                                                                                                                                                                                                            1 GVNAXSSAF 9
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Query Match
Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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A387 junction protein Cx31 - rat

N.Alternate names: connexin-31

C.Species: Rattus norvegicus (Norway rat)

C.Accession: A38737

R.Hoh, J.H., John, S.A.; Revel, J.P.

J. Biol. Chem. 266, 6524-6531, J991

A,Title: Molecular cloning and characterization of a new member of the gap junction gene A,Reference number: A38737; MUID:91177912; PMID:1706719

A,Rocession: A38737

A,Molecule type: DNA

A,Rocession: A38737

A,Rocession: A38737

A,Molecule type: DNA

A,Rocession: A38737

A,Molecule type: DNA

A,Rocession: A38737

A,Rocession: A38737

A,Rocession: A38737

A,Rocession: A38737

                                           A; Molecule type: DNA
A; Residues: 1-529 <WIL>
A; Cross-tacernces: UNIPROT:Q09593; EMBL:Z46935; PIDN:CAA87050.1; GSPDB:GN00020; CESP:M1
A; Experimental source: clone M106
C; Genetics:
A; Genetics:
A; Genetics: 2CSP:M106.3
A; CSP:M106.3
A; Introns: 34/1; 175/3; 224/3; 271/3; 341/3; 372/1; 401/3; 446/3; 475/3; 494/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     urease accessory protein D [imported] - Rhodobacter sphaeroides
C;Species: Rhodobacter sphaeroides
C;Species: Rhodobacter sphaeroides
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C;Accession: 150707
R;Choudhary, M.; Kaplan, S.
Nucleic Acids Res. 28, 862-867, 2000
A;Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides; A;Reference number: Z2522; MuID:20115911; FMID:10648776
A;Recession: T50707
A;Accession: T50707
A;Accession: T50707
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-225 <CHO>
A;Residues: 1-225 <CHO>
A;Residues: 1-225 <CHO>
A;Residues: INTROT:Q9RFF6; EMBL:AF195122; PIDN:AAF24251.1
A;Experimental source: strain 2.4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.9%; Score 30; DB 2; Length 529; 66.7%; Pred. No. 45; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 29; DB 2;
Pred. No. 31;
1; Mismatches
preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 66.7 les 6; Conservative
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Matches
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Zip protein precursor - fruit fly (Drosophila melanogaster)
N.Alternate names: zipper protein
C.Date: 31.Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C.Date: 31.Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C.Date: 31.Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C.Accession: 800483; A37523
EMGO J. 7, 1115-1119, 1989
A.Tele: Zipper encodes a putative integral membrane protein required for normal axon path. A.Teles: Depter encodes a putative integral membrane protein required for normal axon path. A.Teles: Depter encodes a putative integral membrane protein required for normal axon path. A.Teles: South and A.Teles: A.Teles:
C; Keywords: glycoprotein; lysosome, transmembrane protein
F;1-27/Domain: signal sequence #status predicted <516>
F;28-416/Product: lysosomal membrane glycoprotein 1 #status predicted <MAT>
F;28-416/Product: lysosomal lumenal #status predicted <LYS>
F;28-301/Domain: lysosomal lumenal #status predicted <LYS>
F;382-405/Domain: intransmembrane #status predicted <TPWN>
F;406-416/Domain: intransmembrane #status predicted <TPWN>
F;406-416/Domain: intransmembrane #status predicted <TPWN>
F;506-721,102,106,240,249,292,321,379/Binding site: carbohydrate (Asn) (covalent) #status F;107-120,129,144,180,222,227,260/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental F;196/Binding site: carbohydrate (Thr) (covalent) #status experimental F;206,208,210/Binding site: carbohydrate (Ser) (covalent) #status experimental
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hypothetical protein M106.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23740
R;Palmer, S.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19792
A;Accession: T23740
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Pred. No. 42;
0, Mismatches 3; Indels
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Similarity 66.7%;
6; Conservative (
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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C; Accession: USC274
R; Wenzel, K.; Manthey, D.; Willecke, K.; Grzeschik, K.H.; Traub, O.
Bacchen. Biophys. Res. Commun. 248, 910-915, 1998
A.Title: Human gap junction protein connexin31: Molecular cloning and expression analysi A; Reference number: USC274; MUID:98369649; PMID:9704026
A; Accession: USC274
A; Accession: USC274
A; Residues: 1-270 < wmb.>
A; Residues: 1-270 < wmb.>
A; Cross-references: UNIPROT:075712; GB:AJ004856; NID:g3445286; PIDN:CAA06165.1; PID:g344
C; Genetics:
A; Gno: GDB:GJB3
A; Cross-references: GDB:127820
A; Map position: 1p34-1p36
C; Superfamily: gap junction protein
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                                                                                                                                                                                                                                                                                                                                                                                                     Connexin 31 - human
N.Alternate names: gap junction protein beta 3, 31K
C.Species: Homo sapiens (man)
C.Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
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74.4%; Score 29; DB 1; Length 270;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 2; Indels
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74.4%; Score 29; DB 2; Length 270;
Best Local Similarity 66.7%; Pred. No. 38;

Matches 6; Conservative 1; Mismatches 2; Indels
F;185-207/Domain: transmembrane #status predicted <TM4> F;208-270/Domain: intracellular #status predicted <INT3>
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12 GVNQYSTAF 20
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Search completed: October 26, 2004, 16:06:11 Job time: 9.73529 secs

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CAREAGOB3, CAREMBLEAL 27, Created)
02-MAR-2004 (TrEMBLEAL 27, Created)
02-MAR-2004 (TrEMBLEAL 27, Last sequence update)
02-MAR-2004 (TrEMBLEAL 27, Last sequence update)
02-MAR-2004 (TrEMBLEAL 27, Last annotation update)
Possible flagellin and hook associated protein.
FLGL OR RPA0649.
FARGODSeudomonas palustris.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Rhodopseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1] SEQUENCE FROM N.A.
STRAIN-CGA009 / ATCC BAA-98;
PubMed=14704707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAE26093
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09x494 mycoplasma
074f43 geobacter
073586 staphylococ
07a2n4 staphylococ
07a2n4 staphylococ
07a2n4 staphylococ
02e92745 staphyloc
02e92751 staphyloc
02e92751 staphyloc
02e92775 staphyloc
07x3x6 clavibacter
08cyg6 streptocococ
06c733 yarrowia 11
07bsn7 anophales g
06c733 yarrowia 11
07bsn7 anophales g
07xsn mycobacteri
073xm1 mycobacteri
09cc58 mycobacteri
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homo sapien
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                                                                 October 26, 2004, 15:44:50 ; Search time 40.6324 Seconds (without alignments) 127.445 Million cell updates/sec
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Q96140 l
Q7qvj5
Q9brd2 l
Q9np13 l
                                                                                                                                                                                                                            1825181
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                1825181 seqs, 575374646 residues
                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06NC24
CAE26033
QOX454
QOX454
QOX454
QOX424
QOX204
QOX204
QOX306
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Q7PSN7
Q88TX8
Q73XM1
AASO4605
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Gapop 10.0 , Gapext 0.5
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Q922T9
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Q7QVJ5
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1: uniprot_sprot:*
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ининииинииии			7,7	05-JUL-2004 (TrEMBLrel. 27, Last annotation update Possible flagellin and hook associated protein. Name-flgL; OrderedLocusNames-RPA0649;	Rhodopseudomonas palustris. Bactéria; Proteobacteria; Alphaproteobacteria; Rhizobial Bradyrhizobiaceae; Rhodopseudomonas. NCBI TaxID=1076;	0	Signatur=Convoy / ALCL BAA-98; PubMed=14704707; DOI=10.1038/nbt923; Larimer F.W., Chain P., Hauser L., Lamerdin J Land M.L., Pelletter D.A., Beatty J.T., Lang	Bot Har	phocosynimetr Daccettum Knowopseuwomonas palustri Nat. Biotechnol. 22:55-61 (2004). EMEJ. BK572595; 7225693.1; Complete proteome; Flagellum.	MW,				
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ID AAR34096
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"Differential posttrans. Karpas A.B., muhlradt P.F., Wise K.S.;
"Differential posttrans." intraspecies
variation of a major surface lipoprocein and a macrophage-activating
lipopeptide of Mycoplasma fermentans.";
Infect. Immun. 67:760-71(1999).
EMBL; AF100324; AAD25734.1; --
GO; GO:0008152; P:metabolism; IBA.
GO; GO:0008152; P:metabolism; IBA.
InterPro; IPR00188; COrtyor_Metransf.
InterPro; IPR00189; UPF0011.
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Larimer F.W., Chain P., Hauser L., Lamerdin J., Malfatti S., Do L., Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R., Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C., Harrison F.H., Gibson J. Harwood C.S., Torres y Torres J.L., Peres C., Complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodopseudomonas palustris.";
Nat. Biotechnol. 22:55-61(0004).
EMBL, MX772595, CAR26093.11, -.
SEQUENCE 303 AA; 31313 MW; 3243B8F1F30D2CB7 CRC64;
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Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
Geobacteraceae; Geobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycoplasma fermentans.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 87.2%; Score 34; DB 2; Length 303; Best Local Similarity 77.8%; Pred. No. 23; Matches 7; Conservative 1; Mismatches 1; Indels
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236 AA; 26620 MW; F12974232C6E0A35 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Methyl-accepting chemotaxis protein, putative.
ORFNames=GSU0766;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAX-2504 (TrEMBLrel. 26, Last annotation update)
YabC protein.
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TIGRFAMS; TIGR00096; UPF0011; 1.
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Matches 7; Conserv
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STRAIN=PCA / ATCC 51573;
PubMed-14671304; DOI-10.1126/science.1088727;
PubMed-14671304; DOI-10.1126/science.1088727;
Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Salengut J.,
Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
Weidman J.F., Khouri H.M., Fraser C. M.,
Van Aken S.E., Lovely D.R., Fraser C. M.,
"Genome of Geobacter sulfurreducens: metal reduction in subsurface
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Geobacteraceae, Geobacter.
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Pred. No. 1.7e+02;
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Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79920 MW; E61D6ED81FC095C3 CRC64;
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02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
Methyl-accepting chemotaxis protein, putative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00672; HAMP; 1.
Pfam; PF00612; MCPSignal; 1.
SMART; SM0016; HAMP; 1.
PR065TE; SS0111; CHEWOTAXIS_TRANSDUC_2; 1.
PR065TE; PS50865; HAMP; 1.
SEQUENCE 745 AA; 79920 WW; E61D65D81FC09
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TICR; GSU0766; -.
Interpro; IPR004089; Chmtaxis_transd.
Interpro; IPR003660; HAMP.
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Science 302:1967-1969(2003).
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STRAIN=PCA / ATCC 51573;
PubMed=14671304;
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nes 7; Conservative
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22893764DF54BFA7 CRC64;
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InterPro; IPR009229; AgrD.
Pfam; PF05931; AgrD; 1.
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                                       Match 79.5%;
Local Similarity 77.8%;
les 7; Conservative
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ID CAE92745

AC CAE92746;

DT 01-APR-2004 (TrEMBLrel. 27,

DT 01-APR-2004 (TrEMBLrel. 27,

DT 01-APR-2004 (TrEMBLrel. 27,
Complete proteome.
SEQUENCE 47 AA; 5149 MW;
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Lancet 357:1225-1240(2001).
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nes 7; Conservative
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SEQUENCE 47 AA;
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                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=SA502A;
MEDLINE=97342847; PubMed=9197262;
J. G., Beavis R., Novick R.P.;
"Bacterial interference caused by autoinducing peptide variants.";
Science 276:2027-2030(1997).
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Inter-Pro; IPR009229; AgrD.
PEm; PF05931; AgrD; 1.
SEQUENCE 47 AA; 5149 MW; 22893764DF54BFA7 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Name-agrb; OrderedLocusNames=SAV2037;
Stabhylococcus aureus (strain Mu50 / ATCC 700699).
Batchyla, Firmicutes; Bacillales; Staphylococcus.
NCB1_TaxID=158878;
                                                                                                                                             Bacteria; Firmicutes; Bacillales; Staphylococcus. NCBI_TaxID=1280;
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Pred. No. 16;
0; Mismatches
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EMBL, AF0003364; BABBS199.1; -.
InterPro; IPR00929; AgrD.
Pfam; PF05931; AgrD; 1.
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hes 7; Conservative
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                                                                                                                             Name=agrD;
Staphylococcus aureus.
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RESULT 7

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Goorke C., Dashadn S., Kuemmel M., Wolz C.,
Goorke C., Dashadn S., Kuemmel M., Wolz C.,
and cap in Staphylococcus aureus.",
submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ617715, CAE92745.1, -.
SEQUENCE 47 AA, 5149 MW, 22893764DF54BFA7 CRC64,
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SEQUENCE FROM N.A.

SEQUENCE FROM M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Kuroda M., Ohta T., Aoki K.-I., Nagai Y., Lian J.-O., Ito T.,

Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T

Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,

"Whole genome sequencing of meticillin-resistant Staphylococcus
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                                                               Indels
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Q7A417; (TrEMBLrel. 27, Created)

05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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Last annotation update)
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Bacteria; Firmicutes; Bacillales; Staphylococcus
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Bacteria, Firmicutes, Bacillales, Staphylococcus
Score 31; DB 2;
Pred. No. 16;
0; Mismatches
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Query Match 79.5
Best Local Similarity 77.8
Matches 7; Conservative
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CAE92754;
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CAE92757
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Goerke C., Dasbach S., Kuemmel M., Wolz C.;
Goerke C., Dasbach S., Kuemmel M., Wolz C.;
Goerke C., Dasbach S., Tuemmel M., Wolz C.;
and cap in Staphylococcus aureus.";
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; AJG17116; CAE92748.1;
BEQUENCE 47 As, 5149 MM; 22893764DF54BFA7 CRC64;
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01-APR-2004 (TrEMBLrel. 27, Created)
01-APR-2004 (TrEMBLrel. 27, Last sequence update)
01-APR-2004 (TrEMBLrel. 27, Last annotation update)
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Last annotation update)
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NCBI_TaxID=1280;
                         79.5%; Score 31; DB 2;
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                             Query Match 79.5
Best Local Similarity 77.8
Matches 7; Conservative
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CAE92751;
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CAE92751
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CAE9

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RESULT 12

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Goerke C., Dasbach S., Kuemmel M., Wolz C.;
Goerke C., Dasbach S., Kuemmel M., Wolz C.;
Goerke C., Dasbach S., Kuemmel M., Wolz C.;
and cap in Staphylococcus aureus.";
submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases..
EMBL; AJG17718; CAB227541; -.
SEQUENCE 47 AA, 5149 MW; 22893764DF54BFA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=grill-cp8;
Goerke C., Dasbach S., Kuemmel M., Wolz C.;
Goerke C., Dasbach S., Kuemmel M., Wolz C.;
Broultionary Models for the Development of the Polymorphic Loci agr and cap in Staphylococcus aureus.";
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AJG1719; CAE9775-1; -2893764DF54BFA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0MR-2004 (TrEMBLrel. 26, Last annotation update)
Putative tomatinase TomA.
Name=tomA.
Clavibacter michiganensis subsp. michiganensis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococcineae; Microbacteria; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 31; DB 2; Length 47;
Pred. No. 16;
0; Mismatches 2; Indels
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Pred. No. 16;
0; Mismatches 2; Indels
                                                            Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                            Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBL_TaxID=1280;
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                                      01-APR-2004 (TrEMBLrel. 27, 01-APR-2004 (TrEMBLrel. 27, 01-APR-2004 (TrEMBLrel. 27)
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Best Local Similarity 7/...
7/...
7/. Conservative
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                                                                                                       Submitted (UUN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AR393183; AAP57293.1; -.

GO, GO:0004553; F:hydrollase activity, hydrollyzing O-glycosyl . . .; IEA.

GO; GO:0005595; P:carbohydrate meteabolism; IEA.

InterPro; IPR001000; Glyco_hydro_10.

SWART; SM00633; Glyco_hydro_10; 1.

SWART; SM00633; Glyco_l0; 1.

SEQUENCE 543 AA; 58175 MW; BECC284F8A521AED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDINE 21429245; PubMed=11544234;
Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., DeHockins J., Estrem S.T., Fritz L., Full-d., Fullew W., Geringer C., Glamour R., Glass J.S., Knoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P., McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I., Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,
                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glass J.I.;
"Genome of the bacterium Streptococcus pneumoniae strain R6.";
"Genome of the bacterium Streptococcus pneumoniae strain R6.";
J. Bacteriol. 183:5709-5717(2001).
EMBL; AE0089518; AAL00300.1; -.
PIR; G98058; G98058.
GO; G0:0016020; C:membrane; IEA.
InterPro; IRR00388; DUF214.
Pfam; PP02687; PtaX; 2.
Complete proteome; Hypothetical protein.
SEQUENCE 924 AA; 102967 WW; 192383CF91548592 CRC64;
                                                                                                                                                                                                                                                                                 Query Match
Post Local Similarity. 66.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.5%; Score 31; DB 2; Length 924; 66.7%; Pred. No. 3.6e+02; tive 2; Mismatches 1; Indels
                                                     STRAIN-NCPPB382;
Gartemann K.-H., Graefen I., Zellermann E.-M., Burger A.,
Eichenlaub R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UNH-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein spr1496.
OrderedLocusNames=spr1496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            924 AA.
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Best Local Similarity 66.7
Matches 6; Conservative
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239 GLNAFSSAY 247
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NCBI_TaxID=33013;
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Q8CYG6
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Search completed: October 26, 2004, 16:05:07 Job time : 42.6324 secs

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S. aureus Staphyloc Staphyloc Human kin Human leu Peptide-m

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Protected AgrD2 lin AgrD2 lin AgrD-auto

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The present sequence represents a cyclic peptide which is a modulator of the agr response. Agonists of this response antagonize early stages of virulence, specifically production of cell wall proteins (so are preferred for prophylaxis), while antagonists interfere with the later
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/note= "linked by -O-CH(NHX)-(CH2)n-S, where X is
comprises 2-5 amino acids, and is not Gly-Val-Asn-Ala
(claim 1) or is Gly-Val-Asn-Ala (claim 8)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for treating and preventing bacterial
Aay67851
Aay67852
Aay67853
Aay67853
Aay67859
Abb97454
Abb97159
Abb07160
Aam51001
Aam51004
Aam51005
Aam51003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibacterial cyclic oligopeptide for Staphylococcus strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cyclic peptide, modulator, agr response; virulence, cell wall protein production; prophylaxis; exotoxin secret bacterial infection; toxic shock syndrome; Staphylococci; Staphylococcus aureus; coagulase negative S. epidermidis; medical implant infection; cyclic.
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                                                                                                                                                                                                                                                                                                     ALIGNMENTS
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AAX67851
AAX67862
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AAY67863
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ABB07159
ABB07159
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  (first entry)
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Key
Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                             13-AUG-1999
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  Synthetic.
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 AgrD-auto
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S. aureus
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Aay67858 S. aureus
Aam50906 AgrD-auto
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                                                                                           ; Search time 23.75 Seconds (without alignments) 75.522 Million cell updates/sec
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Add11974
Aav21519
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Aay67854
Aay67860
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              5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                        hits satisfying chosen parameters:
                                                                                                                                                                                                                                               2002273 segs, 358729299 residues
              GenCore version
Copyright (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                  sw model
                                                                                              October 26, 2004, 15:44:15
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11: geneseqp1980s:*
2: geneseqp1990s:*
4: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2003s:*
6: geneseqp2003bs:*
8: geneseqp2003bs:*
                                                                  protein search, using
                                                                                                                                                                                                                                                                                                   seq length: 0 seq length: 2000000000
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Maximum DB
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Result

Gaps

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0; Indels

1.7e+06;

94.7%; Score 100.0%; Pred. No. 1... 0; Mismatches

Conservative

4.

2 SSLF 5

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Query Match Best Local Similarity Matches 4; Conserv

Score 18; DB 3;

Staphylococcus aureus; AgrD; agr response; inhibitor; antibiotic; antibacterial; infection; therapy; cyclic.

AgrD-autoinducing cyclic peptide, inhibitor of agr response.

08-MAY-2002

AAM50906;

AAM50906 standard; peptide; 5 AA.

RESULT 3 AAM50906

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stages of virulence, specifically secretion of exotoxin (so are preferred for treatment). The peptides are used to treat or prevent bacterial infections in humans and animals, also for incorporation into medical articles, e.g tampons (to prevent toxic shock syndrome), prostheses and wound dressings. Particularly they are active against staphylococci, specifically Staphylococcus aureus but also coagulase-negative S. epidermidis, implicated in infection of medical implants. note: this sequence does not appear in the specification; it was created using information provided
                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a cyclic peptide derived from the Staphylococcus aureus AgrD peptide. The invention relates to AgrD derived peptides, a composition containing a peptide and a carrier, and a method for the production of the cyclic peptides. The peptide inhibits the agr response, which is normally associated with the release of virulence factors of Staphylococcus aureus. An AgrD peptide is produced by S. aureus that activates the agr response in strains of a single group, but interferes with this response in strains of different groups. The peptides and composition containing them can be used to treat infections by S. aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New cyclic peptides for treating infections with Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "N-terminal residue is linked to the C-terminal residue to form a cyclic peptide"
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus infection; cyclic peptide; AgrD; agr response; virulence factor; treatment.
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                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                               Length 4;
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100.0%; Pred. No. 1.7e+06;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                     AAY67858 standard; peptide; 5 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Unknown
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(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                               2 SSLF 5
                                                                                                                                                                                              Sequence 4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
AAY67858
                    888888888888888
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The present sequence is that of a novel synthetic cyclic peptide of the invention that is capable of inhibiting the agr response of staphylococcus aureus. It is an AgrD-aucoinducing peptide, where AgrD is a secreted agr-encoded peptide and where the agr locus controls the ascreted agr-encoded peptide and where the agr locus controls the synthesis of virulence factor and other extracellular proteins

CC synthesis of virulence factor and other extracellular proteins

CC responsible for pathogenicity in S. aureus. Preferred peptides may have the sequence NH2-Xin)-Z-X(y)-CCOM, with a cyclic bond between the Z residue and COOH other than a thioester bond, where X is an amino acid, an amino acid analogue, a peptidomimetic or non-amide isostere, Z is a synthetic or a biosynthetic amino acid, n is 0-10 and y is 1-10. The cyclic bond is especially a lactam or lactone bond. The thiololactone contractive within native AgrD peptides is required for activation of the agr response. Blimination of the thiol ester component of the cyclic ring structure can destroy agr response activating activity while preserving and enhancing inhibitory activity. A claimed method of preparing a cyclic peptide involves: assembling a linear peptide chain on to a solid phase creating the deprotecting the resulting protected assembled peptide involves: assembling a linear peptide chain on to a solid phase creating the deprotected peptide and cleave the peptide from the support; and recovering the cyclic peptide. The peptide is useful for
                                                                                                                                                                                                                                                                                'note= "note linked to residue 5 to form cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                             /note= "note linked to residue 1 to form cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel synthetic, cyclic AgrD-autoinducing peptide for bacterial interference and for treating Staphylococcus aureus infection in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novick RP, Beavis R,
                                                                                                                                                                                                                                                                                                                      'note= "any amino acid"
                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Col 19; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-00339511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0090402P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYNQ ) UNIV ROCKEFELLER.
(UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muir TW, Mayville P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-170774/22.
                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                          Misc-difference
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                                                                                                                                                                                                   Synthetic
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Sequence 5 AA;

(first entry)

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ADD11974 standard; peptide; 5 AA.
                                                                                01-JAN-2004
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                                                             ADD11974;
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                       RESULT 5
                                  ADD11974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP53540 to ABP53547 represent cyclic peptides (I) from the present invention. The present invention also describes a method for treating Staphylococcus aureus infection comprising the administration of a composition comprising (I). (I) has antibacterial activity, and can be used as an agr gene response inhibitor. The peptides are useful for treating S. aureus infections
                                                                       Gaps
bacterial interference, especially for the treatment of S. aureus infection
                                                                                                                                                                                                                                    Cyclic peptide; Staphylococcus aureus; infection; antibacterial; agr response inhibitor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cyclic peptides, useful for treating Staphylococcus aureus
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                                                    Length 5;
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                                                  94.7%; Score 18; DB 5; Len
100.0%; Pred. No. 1.7e+06; ··
ive 0; Mismatches 0;
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100.0%; Pred. No. 1.7e+06;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beavis
                                                                                                                                                                                                                                                                                                        /note= "any amino acid"
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                                                                                                                                                         ABP53547 standard; peptide; 5
                                                                                                                                                                                                                                                                                                                                                                27-DEC-2001; 2001US-00032950.
                                                                                                                                                                                                                                                                                                                                                                                  98US-0090402P.
                                                                                                                                                                                                                   Cyclic peptide SEQ ID NO:8
                                                                                                                                                                                                (first entry)
                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mayville P,
                                                                                                                                                                                                                                                                                                                                                                                                              MUIR T W.
MAYVILLE P.
NOVICK R P.
BEAVIS R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-681366/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 4; Conserv
                                                            Local Similarity
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Misc-difference
                                                                                         'n.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 AA;
                                Sequence 5 AA;
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                                                                                                                                                                                                                                                                                                                                             20-JUN-2002
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                                                                                                                                                                             ABP53547;
                                                                                                                                                                                                                                                                  Synthetic
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                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                        (MAYV/) N
(NOVI/) 1
(BEAV/) E
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                                                            Best Loc
Matches
                                                                                                                                        RESULT 4
                                                                                                                                                  ABP53547
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The invention relates to a novel modulator of binding between a PDZ protein (post-synaptic density protein (20-1) and a PDZ ligand (PL) protein and Sonula Goccludin 1 protein (20-1) and a PDZ ligand (PL) protein. The modulator is a peptide having 3 residues of a C-terminal sequence of a PL protein. PDZ and PL proteins are a binding pair given in specification, or a peptide mimetic of the 3 residues PL protein or a sequence of a PL protein. PDZ and PL proteins are a binding pair given in specification, or a peptide mimetic of the 3 residue PL protein, or a mall molecule having similar functional activity as the 3 residue PL protein. The reagents of the invention have the following activities: antiminflammatory, antiallergic, antiulor, antighorhatic, osteopathic, a chiminflammatory, and immunomodulator. The movel modulator is useful for treating a disease correlated with binding between a PDZ protein and PL protein. The disease cor cancer. The modulator is useful for modulating vesicular trafficking, tumour suppression, signal transcendence of immune response and organisation of synapse formation. The modulator is useful for facilitating the assembly of multiprotein complexes, often serving as a bridge between several proteins, or regulation of immune response and to inhibit leukocyte activation. The modulator is useful for treating diseases characterised by inflammatory and humoral immune response e.g., inflammatory asthma, allergy, inflammatory bowel diseases, ulcerative colitis, psoriasis, asthma, allergic thinits, aropic dermatiis, arthritis, anthia, arbeits, graft-versus-host diseases, atherosclerosis,
                                                                                          modulator, PDZ; post-synaptic density protein 95, PSD95; Dobosophila large disc protein; Zonula Occiduin 1 protein; Zo-1; PDZ ligand; PL; antiinflammatory; antiallargic; antiulcer; antipsoriatic; antiasthmatic; dermatological; neuroprotective; virucide; antidiabetic; osteopathic; antiarthritic; immunosuppressive; antiatherosclerotic; cytostatic; anti-HIV; vasotropic; immunomodulator; neurological disease; immune response disease; muscular disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDZ and
                                                                                                                                                                                                                                                                                                                                                                                                                                    modulating vesicular trafficking; tumour suppression; signal transduction; protein sorting; membrane polarity; apoptosis; synapse formation; multi-protein complex; leukocyte activation inhibitor; cell adhesion molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modulator of binding between discs-large homology repeat protein, IPDZ ligand protein, is a peptide having few residues of C-terminal sequence of PDZ ligand protein.
Cell adhesion molecule PL protein C-terminal core peptide #277.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schweizer J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 35; 172pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-AUG-2001; 2001US-0309841P.
25-FEB-2002; 2002US-0360061P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-AUG-2002; 2002WO-US024655
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Indels

Conservative

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Alternatively, it can be synthesised by solid-phase techniques. One or both of the Ser residues at positions 1 or 2 may be absent. The peptide can be used in biological studies for the development of drugs. See also AAR10516-R10518 and AAR10520. (Updated on 27-AUG-2003 to correct OS
leukaemia, infectious diseases (viral infection such as human immunodeficiency virus (HIV)), and ischaemia. This sequence represents a PL protein C-terminal core peptide of a cell adhesion molecule of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muscular contraction-inhibitory neuro-peptide(s) in mollusca - prepd. by purifying oligopeptide using high power lig. chromatography after extracting neuro:ganglion of Fusinus perplex ferrigineus.
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                              muscular contraction-inhibitory neuropeptide; FIPB1; Mollusca; radular tractile muscle.
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94.7%; Score 18; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                           0; Indels
                                                                                                                           94.7%; Score 18; DB 7; Length 5; 100.0%; Pred. No. 1.7e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                      AAR10519 standard; protein; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 1; 10pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                   Fusinus inhibitory peptide Bl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89JP-00125596.
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                                                                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
                                                                                                                         Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusinus ferrugineus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SUNR ) SUNTORY LID.
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                                                                                                                                                                                           2 SSLF 5
                                                                                                                                                                                                                          SSLF 4
                                                                                              Sequence 5 AA;
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15-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-DEC-1990
                                                                                                                                                                                                                                                                                                                                       AAR10519;
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                                                                                                                                                                                                                                                                         RESULT 6
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                8833333
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This sequence represents a synthetic ferritin peptide which was used as a functional surrogate in the conjugate of the invention. The novel

C labelled conjugate comprises at least one label attended to a functional surrogate of an analyte of interest. The surrogate is capable of competing effectively with the analyte for a limiting amount of an effinity receptor for the analyte. The conjugate exhibits an activity that is altered upon interaction with the affinity receptor and this activity can be measured and related to the amount of the analyte present in a sample. Functional surrogates such as this have an immunorsactive or analyte for a limiting amount of its affinity receptor and this analyte for a limiting amount of its affinity receptor. Functional surrogate to compete effectively and with the analyte for a nalyte for analyte competitive affinity receptor. Functional surpastes are able to mamic naturally occurring analytes. They can be surrogates are able to mamic naturally occurring analytes. They can be surrogates are able to ompetitive affinity assays (esp. homogenous immunoassays) for detecting large macromolecules such as polymepties, polymucleoties, glycoproteins and lipid-containing confection include cardiac or tumour markers, allergens, hormones related to fertility-pregnancy or analytes associated with infectious disease. In detection include cardiac or tumour markers, allergens, hepatitis antigens or antibodies against them, human chorionic gonadotropin, human luteinising hormone, human placental lactogen, hepatitis antigen cardinomer, promone, human placental lactogen, hepatitis antigen cor toxoplasma, herpes virus, DK-MB, myoglobin, myosin light chain, troponin, cardinoembryonic antigen, alpha-fetoprotein, prostate-specific antigen and GA125 (a tumour marker). (Updated on 25-MAR-2003 to correct Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Labelled functional surrogate of an analyte - useful as competitor molecule in affinity assays, esp. for detecting large macromolecules such
                                                                                                                                                                               Functional surrogate; analyte; affinity receptor; immunoreactive group; mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia; cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin; pregnancy; infectious disease; ferritin; myosin light chain; troponin; follicle stimulating hormone; human; growth hormone; immunoglobulin E; prolactin; parathyroid hormone; placental lactogen; hepatitis antigen; antibody; chorionic gonadotropin; luteinising hormone; cytomegalovirus; Streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen; carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 51; Page 27; 156pp; English.
                                                                                                                                       Synthetic ferritin peptide #28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-00476375.
                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carter JM;
                                                                   (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTO-) CYTOGEN CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9641172-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1996;
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                                                                 25-MAR-2003
10-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as ferritin.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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Gaps .

0; Indels Length 6;

94.7%; Score 18; DB 2; Le 100.0%; Pred. No. 1.7e+06; iive 0; Mismatches 0;

Query Match
Best Local Similarity 100.
Matches 4; Conservative

AAW25555 standard; peptide; 6 AA.

AAW25555 ID AAW

RESULT 7

SSLF 5

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SSLF

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Sequence 6 AA;

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This sequence represents a peptide motif derived from ferritin which is important for selective binding affinity. Peptides containing motifs such as this may be used as functional surrogates in the conjugate of the invention. The novel labelled conjugate comprises at least one label attached to a functional surrogate of an analyte of interest. The surrogate is capable of competing effectively with the analyte for a limiting amount of confusition of the conjugate of competing effectively with the analyte for a limit in a sample. Functional surrogates such as this have confusitive present in a sample. Functional surrogates such as this have an immunoreactive group that allows the surrogates compete effectively of the analyte for a limiting amount of its affinity receptor. Functional surrogates are able to mimic naturally occurring analytes. They can be labelled for use in standard competitive affinity assays (egp. homogenous immunoassays) for detecting large macromolecules such as polymented cardiac or tumont markers, allergens, containing macromolecules, polymucleotides, glycoproteins and lipid-containing macromolecules, swell as well as small haptens. Typical diagnostic containing macromolecules, polymucleotides, glycoproteins and lipid-containing macromolecules, as well as small as small haptens. Typical diagnostic containing macromolecules, as well as small as small haptens. Typical diagnostic containing macromolecules, whuman growth hormone. Infectious disease. In particular, the assays are useful for detecting ferritining hormone, human placental competition includes or analytes associated with the municular, parathyroid hormone, human placental competition includes against them, human chorionic gonadotropin, human luteinising hormone, cytomegalovirus, Chlamydia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Labelled functional surrogate of an analyte - useful as competitor molecule in affinity assays, esp. for detecting large macromolecules such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Functional surrogate; analyte; affinity receptor; immunoreactive group; mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia; cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin; pregnancy; infectious disease; fertitin; myosin light chain; troponin; follicle stimulating hormone; human; growth hormone; immunoglobulin E; prolactin; parethyroid hormone; placental lactogen; hepatitis antigen; antibody; chorionic genadotropin; luteinising hormone; cytomegalovirus; Streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen; carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ferritin motif #26 important for selective binding affinity.
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                                                                                                                                                                                                                                                                                                                        AAW10783 standard; peptide; 6 AA.
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10-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Labelled functional surrogate of an analyte - useful as competitor molecule in affinity assays, esp. for detecting large macromolecules such
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Streptococcus a, rubella, toxoplasma, herpes virus, DX-MB, myoglobin, myosin light chain, troponin, carcinoembryonic antigen, alpha-fetoprotein, prostate-specific antigen and CA125 (a tumour marker), (Updated on 25-MAR-2003 to correct PI field.)
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                                                                                                                                         Length 6;
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Pred. No. 1.7e+06;
                                                                                                                           94.7%; Scor. 100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                   AAW25549 standard; peptide; 6 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic ferritin peptide #22.
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Best Local Similarity
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                                                                                                  Sequence 6 AA;
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10-NOV-1997
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polysaccharides, polynucleotides, glycoproteins and lipid-containing macromolecules, as well as small haptens. Typical diagnostic analytes for detection include cardiac or tumour markers, allergens, hormones related to fertility-pregnancy or analytes associated with infectious disease. In particular, the assays are useful for detecting ferritin, follicle particular, the assays are useful for detecting ferritin, follicle particularing hormone, human placental lactogen, hepaticis antigens or antibodies against them, human chorionic gonadortorpin, human luteinising hormone, cytomegalovitus, Chlamydia, Streptococcus a, rubella, toxoplasma, herpes virus, DR-MB, myoglobin, myosin light chain, troponin, and Call25 (a tumour marker). (Updated on 25-MAR-2003 to correct PI
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ID AAW25550
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functional surrogate in the conjugate of the invention. The novel labelled conjugate comprises at least one label attended to a functional surrogate of an analyte of interest. The surrogate is capable of competing effectively with the analyte. The surrogate is capable of affinity receptor for the analyte. The conjugate exhibits an activity that is altered upon interaction with the affinity receptor and this conjugate in a sample. Functional surrogates such as this have an immunoreactive in a sample. Functional surrogates such as this have an immunoreactive crowp that allows the surrogate to compete effectively and with the surrogates are able to mimic naturally occurring analytes. They can be labelled for use in standard competitive affinity assays (esp. homogenous communicates are able to mimic naturally occurring analytes. They can be labelled for use in standard competitive affinity assays (esp. homogenous communicates, so well as small haptens. Typical diagnostic analytes for detecting large macromolecules, as well as small haptens. Typical diagnostic analytes for detecting include cardiac or tumour markers, allergans, hormones related to fartility-pregnancy or analytes associated with infectious disease. In particular, the assays are useful for detecting ferritin, follicle cardinal hormone, human placental lactogen, hepatitis antigens or antibodies against them, human chorionic gonadotrophi, human luteinising to cormone, cytomegalovirus, Chlamydia, Streptococcus a, rubella, toponin, toxomone, cytomegalovirus, Chlamydia, Streptococcus a, rubella, cardingen, alpha-fecoprolein, prostate-specific antigen and CALS (a tumour marker). (Updated on 25-MAR-2003 to correct PI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                signal transduction; protein sorting; membrane polarity; apoptosis; synapse formation; multi-protein complex; leukocyte activation inhibitor; cell adhesion molecule.
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25-FEB-2002; 2002US-0360061P.
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Matches 4; Conserv
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96WO-US010498. 95US-00476375.

07-JUN-1996; 07-JUN-1995;

WO9641172-A1

Synthetic.

19-DEC-1996.

PDZ and

Carter JM;

Lee-Owen FV,

WPI; 1997-077284/07.

(CYTO-) CYTOGEN CORP.

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The invention relates to a novel modulator of binding between a PDZ protein (poer-synaptic density protein 95 (PSD95), Drosophila large disc protein and Zonula Occludin 1 protein (20-1)) and a PDZ ligand (PL) correction. The modulator is a peptide having 3 residues of a C-terminal sequence of a PL protein. PDZ and PL proteins are a binding pair given in specification, or a peptide mimetic of the 3 residue PL protein, or a mail molecule having similar functional activity as the 3 residue PL protein. The reagents of the invention have the following activities: continflammatory, antiallergic, antiulcer, antiquabetic, osteopathic, antiarthratic, immunosuppressive, antiathercollerctic, osteopathic, antiarthratic, immunosuppressive, antiathercollerctic, oytostatic, anti-Y, vasotropic, and immunomodulator. The modulator is useful for treating a disease correlated with binding between a PDZ protein and PL protein. The disease correlated with binding between a PDZ protein and PL protein. The disease correlated with binding between a PDZ protein and PL protein. The disease can be a neurological disease, immune response disease, muscular disease can be a neurological disease, immune response correlator. The modulator is useful for facilitating the assembly of multicanduction. The modulator is useful for facilitating the assembly of multicant protein complexes, of the serving as a bridge between several proteins, or regulating the function of immune responses e.g., inflammatory bowel diseases, ulcerative colitis, psoriasis, asthma, allergy, inflammatory bowel diseases, ulcerative colitis, psoriasis, allergy, inflammatory bowel diseases, ulcerative colitis, asthma, allergy, inflammatory bowel diseases, ulcerative colitis, asthma, leaves and inflammatory bowel diseases, ulcerative colitis, psoriasis, allergy, inflammatory bowel diseases, ulcerativity colitis, astopic dermatitis, arthritis, atopic dermatitis, arthritis, astopic dermatitis, astopic dermatitis, astopic dermatitis, astopic dermatitis, astopic dermaticien colimun
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                                                                                              Modulator of binding between discs-large homology repeat protein, 1
PDZ ligand protein, is a peptide having few residues of C-terminal
sequence of PDZ ligand protein.
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     Carrick DM;
     Schweizer J,
                                                                                                                                                                                                        Disclosure; Page 35; 172pp; English.
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(first entry)
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  Rabinowitz JD,
                                                   WPI; 2003-268193/26.
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This sequence represents a peptide motif derived from ferritin which is important for selective binding affinity. Peptides containing motifs such as this may be used as functional surrogates in the conjugate of invention. The novel labelled conjugate comprises at least one label curvantion. The novel labelled conjugate comprises at least one label curvantion. The novel labelled conjugate comprises at least one label curvantion. The novel labelled conjugate compression and this activity that is altered upon interaction with the analyte for a limiting amount of interest of an immunoreactive group that allows the surrogates such as this have considered to be amount of the analyte present in a sample. Functional surrogates such as this have an immunoreactive group that allows the surrogates such as this have considered for a limiting amount of its affinity receptor. They can be labelled for use in standard competitive affinity assays (esp. homogenous immunoassays) for detecting large macromolecules, as well as small laptens. Typical diagnostic containing macromolecules, as well as small laptens. Typical diagnostic containing macromolecules, as well as small haptens. Typical diagnostic ferritin, follicle stimulating hormone, human growth hormone, containing macroplecular, the assays are useful for detecting infectious disease. In particular, the assays are useful for detecting carciborin, human lutelnising hormone, cytomegalovirus, Chlamydia, Streptococcus an rubella toxoplasma, herpes virus, DK-MB, myoglobin, cytopoin, troponin, carcinoembryonic antigen, altimuter, proponin, carcinoembryonic antigen, altimuter, proponin, carcinoembryonic antigen, altimuter, proponin, carcinoembryonic antigen, altimuter. Proponin, carcinoembryonic antigen,
                                                                                                                                                                                                                                                                                                                                              Labelled functional surrogate of an analyte - useful as competitor molecule in affinity assays, esp. for detecting large macromolecules such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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100.0%; Pred. No. 1.7e+06;
cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 56; Page 56; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW10801 standard; peptide; 7 AA.
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(first entry)
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Best Local Similarity 100.v
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10-NOV-1997
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Gaps

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Labelled functional surrogate of an analyte - useful as competitor molecule in affinity assays, esp. for detecting large macromolecules such Functional surrogate; analyte; affinity receptor; immunoreactive group; mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydla; cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin; pregnancy; infectious disease; ferritin; myosin light chain; troponin; follicle stimulating hormone; human; growth hormone; immunoglobulin E; prolactin; parathyroid hormone; placental lactogen; hepatitis antigen; antibody; chorionic gonadotropin; luteninising hormone; cytomegalovirus; Streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen; carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125. Claim 56; Page 56; 156pp; English. 96WO-US010498. 95US-00476375. (CYTO-) CYTOGEN CORP. WPI; 1997-077284/07 Lee-Owen FV, WO9641172-A1. 07-JUN-1996; ferritin. 19-DEC-1996. Synthetic.

```
This sequence represents a peptide motif derived from ferritin which is important for selective binding affinity. Peptides containing motifs such as this may be used as functional surrogates in the conjugate of the invention. The novel labelled conjugate comprises at least one label attached to a functional surrogate of an analyte of interest. The currogate is capable of competing effectively with the analyte for a limiting amount of an affinity receptor for the analyte. The conjugate exhibits an activity that is altered upon interaction with the affinity receptor and this activity can be measured and related to the amount of the analyte present in a sample. Functional surrogates such as this have an immunoreactive group that allows the surrogate to compete effectively receptor. They can be labelled for a limiting amount of its affinity receptor. They can be labelled for use in standard competitive affinity assays (esp. homogenous immunoassays) for detecting large macromolecules such as well as swall as small appens. Typical diagnostic containing macromolecules, as well as small haptens. Typical diagnostic analytes for detection include cardiac or tumour markers, allergens, infectious disease. In particular, the assays are useful for detecting lacticity infectious disease. In particular, the assays are useful for detecting contacting macromolecules, as well assays are useful for detecting streptococcus and intensive normal process related to fertility-pregnancy or analytes associated with the infectious disease. In particular, the assays are useful for detecting streptococcus as rubbaticis antigens or antibodies against them, human consider a rubballar, toxoplasma, herpes virus, DK-MB, myoglobin, myosin light chain, troponin, carcinoemberone, antigen, alpha-coccus and rubbatic antigen and CANZS (a tumoroccus).
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94.7%; Score 18; DB 2; Length 7; 100.0%; Pred. No. 1.7e+06; 0; Indels 100.0%; Preq. ... 4; Conservative Query Match Best Local Similarity Sequence 7 AA; Matches

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Gaps

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2 SSLF 5

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RESULT 14

AAW10784 standard; peptide; 7 AA AAW10784

AAW10784;

(revised)
(first entry) 25-MAR-2003 10-NOV-1997

Ferritin motif #27 important for selective binding affinity.

minic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia, cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin; pregnancy; infectious disease; ferritin; myosin light chain; troponin; follicle stimulating hormone; human; growth hormone; immunoglobulin E; prolactin; parathyroid hormone; placental lactogen; hepatitis antigen; antibody; chorionic gonadotropin; luteninsing hormone; cytomegalovirus; Streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen; carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125. Functional surrogate, analyte, affinity receptor, immunoreactive group,

Synthetic.

WO9641172-A1.

19-DEC-1996.

96WO-US010498. 07-JUN-1996;

95US-00476375. 07-JUN-1995;

(CYTO-) CYTOGEN CORP.

Lee-Owen FV,

Carter JM;

WPI; 1997-077284/07.

Labelled functional surrogate of an analyte - useful as competitor molecule in affinity assays, esp. for detecting large macromolecules such as ferritin.

Claim 51; Page 56; 156pp; English.

This sequence represents a peptide motif derived from ferritin which is important for selective binding affinity. Peptides containing motifs such as this may be used as functional surrogates in the conjugate of the invention. The novel labelled conjugate comprises at least one label attached to a functional surrogate of an analyte of interest. The attached is competing effectively with the analyte for a limiting amount of an affinity receptor for the analyte. The conjugate exhibits an activity that is altered upon interaction with the affinity receptor for the analyte present in a sample. Functional surrogates such as this have an immunoreactive group that allows the surrogate to compete effectively an immunoreactive group that allows the surrogate to compete effectively and with the analyte for a limiting amount of its affinity receptor. They can be labelled for use in standard competitive affinity assays to proceed an immunosassays) for detecting large macromolecules such as well as well as small haptens. Typical diagnostic containing macromolecules, as well as small haptens. Typical diagnostic analytes for detection include cardiac or tumour markers, allergens, containing macromolecules, as well as small haptens. Typical diagnostic ferritin, follicle stimulating hormone, human growth hormone, commone, human chorionic genadotropin, human luteinising hormone, cytomegalovirus, Chlamydia, composin, prostate-specific antigen and CALLS (a tumour marker).

Streptococus as rubbella, toxoplasma, herpes virus, DK-MB, myoglobin, myosin light chain, troponin, carcinoembryonic antigen, alpha-feroproperin, prostate-specific antigen and cargin captions.

Sequence 7 AA;

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This sequence represents a peptide motif derived from ferritin which is important for selective binding affinity. Peptides containing motifs such as this may be used as functional surrogates in the conjugate of the invention. The novel labelled conjugate comprises at least one label attached to a functional surrogate of an analyte of interest. The surrogate is capable of competing effectively with the analyte for a limiting amount of an affinity receptor for the analyte. The conjugate exhibits an activity that is altered upon interaction with the affinity receptor and this activity can be measured and related to the amount of the analyte present in a sample. Functional surrogates such as this have an immunoractive group that allows the surrogate to compete effectively and with the analyte for a limiting amount of its affinity receptor. Functional surrogates are able to mimic naturally occurring analytes. They can be labelled for use in standard competitive affinity assays (esp. homogenous immunoassays) for detecting large macromolecules such as polyapptides, polyacacharides, polynucleotides, glycoproteins and lipid-containing macromolecules, as well as small haptens. Typical diagnostic analytes for detection include cardiac or tumour markers, allergens, therabet to fertility-pregnancy or analytes associated with infectious disease. In particular, the assays are useful for detecting ferritin, follicle stimulating hormone, human growth hormone,
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Functional surrogate; analyte; affinity receptor; immunoreactive group; mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia; cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin; pregnancy; infectious disease; ferritin; myosin light chain; troponin; follicle stimulating hormone; human; growth hormone; immunoglobulin B; prolactin; parathyroid hormone; placental lactogen; hepatitis antigen; antibody; chorionic gonadotropin; luteinising hormone; cytomegalovirus; Streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen; carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.
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    Length 7;
                                            0; Indels
DB 2; Le
1.7e+06;
Query Match 94.7%; Score 18; DB Best Local Similarity 100.0%; Pred. No. 1.7 Matches 4; Conservative 0; Mismatches
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                                                                                                                                                                                                                                          AAW10779 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96WO-US010498
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10-NOV-1997
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cc immunoglobulin E, prolactin, parathyroid hormone, human placental cc lactogen, hepatitis antigens or antibodies against them, human chorionic gonadotroph, human luteinising hormone, cytomegalovitus, Chlamydia, CC Streptococcus a, rubella, toxolasma, herpes virus, DK-MB, myoglobin, myosin light chain, troponin, carcinoembryonic antigen, alphacc fetoprotein, prostate-specific antigen and CA125 (a tumour marker).

CC (Updated on 25-MAR-2003 to correct PI field.)

XX

SQ Sequence 7 AA;

Query Match

Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SSLF 5

Cy 2 SSLF 5

Bbb 3 SSLF 6

Search completed: October 26, 2004, 15:59:47
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9, Appli 31, Appl 5, Appli 289, App 289, App

Sequence

Sequence 5, Apply Sequence 289, Apply Sequence 59, Appli Sequence 59, Appli Sequence 59, Appli Sequence 288, Apply Sequence 3111, Apply Apply Sequence 3111, Apply Se

Sequence 88, Appl Sequence 88, Appl Sequence 88, Appl Sequence 40860, A Sequence 28, Appl

Sequence 288, A Sequence 288, A Sequence 319, A Sequence 311, A Sequence 89, Ap

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Gaps

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APPLICANT: Muir, Tom
APPLICANT: Mayuille, Patricia
APPLICANT: Mayuille, Patricia
APPLICANT: Mayuille, Patricia
APPLICANT: No. US2002007453Alick, Richard P.
APPLICANT: Beavis, Ronald
APPLICANT: Beavis, Ronald
APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
CURRENT PAPLICATION NUMBER: 000-1-2-31
PRIOR APPLICATION NUMBER: 60/090,402
PRIOR PLILING DATE: 1998-06-24
NUMBER OF SEO ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , LOCATION: (1)
, OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-8
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94.7%; Score 18; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels
6. US-10-706-391-42
6. US-10-706-391-43
6. US-10-706-391-43
6. US-10-174-613-31
6. US-10-174-613-31
6. US-10-174-613-31
7. US-10-367-593-289
7. US-10-367-593-289
7. US-10-367-594-289
7. US-10-367-684-289
7. US-10-367-684-289
7. US-10-367-684-289
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7. US-10-367-684-289
7. US-10-367-684-289
7. US-10-367-683-68
7. US-10-367-683-88
7. US-10-367-684-288
7. US-10-365-864-1613
7. US-09-864-761-4860
7. US-09-864-761-4860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/10032950; Publication No. US20020077453A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ 1D NO 8
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
     10-032-950-8
       à
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Sequence 13, App
Sequence 17, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 470, Appli
Sequence 12, Appli
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                                                                                               October 26, 2004, 15:54:00 ; Search time 17.5 Seconds (without alignments) 92.502 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications AA:*

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                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 US-10-022-950-8
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3 US-10-032-950-1
3 US-10-032-950-2
3 US-10-032-950-3
1 US-10-032-950-4
1 US-10-032-950-4
1 US-10-022-066-266
1 US-10-22-066-266
1 US-10-29-086-12
US-10-293-086-12
US-10-293-086-12
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                                                                                                                                                                                                                                                        1364641 seqs, 323758627 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                        - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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APPLICANT: MAYAILE, Patricia
APPLICANT: MAYAILE, Patricia
APPLICANT: MAYAILE, Patricia
APPLICANT: MAYAILE, Ronald
APPLICANT: Beavis, Ronald
APPLICANT: Beavis, Ronald
APPLICANT: Di, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: NOTER: STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: NOTER: US/10/032,950
CURRENT APPLICATION NUMBER: US/10/032,950
CURRENT FILING DATE: 1099-06-24
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 1
LENGTH: 9
LENGTH: 9
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; OTHER INFORMATION: Xaa represents any amino acid at this position.
US-10-032-950-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 9;
         Patentin Release #1.0, Version #1.30
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Pred. No. 1.2e+06;
                                                                    FILING DATE: 07-May-200
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: US 09/073,898
FILING DATE: 06-May-1998
APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-OCT-1997
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1996
ATTORNEY AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REGISTRATION NUMBER: 39,355
REGISTRATION NUMBER: 39,355
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/850,351A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: .67:
US-09-850-351A-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/10032950 Publication No. US20020077453A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Best Local Similarity
Matches 4; Conserva
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Loewer, David
Dullum, Charles Joseph
Muller-Cohn, Judy
Stamp, Lisa
Morrill, George
TITLE OF INVENTION: No. US20020100080A1el Pesticidal Toxins and Nucleotide
Sequences Which Encode These Toxins
                                                                                                                                                                                                APPLICANT: HIDDERAND, WILLIAM H.
APPLICANT: PRILLIMAN, KILEY RAE
TITLE OF INVENTION: METHOD AND APPRACTUS FOR THE PRODUCTION OF ANTIGENS AND
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 6680.034
CURRENT PAPLICATION NUMBER: 09/10/022,066
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/256,410
PRIOR APPLICATION NUMBER: 60/256,409
PRIOR PILING DATE: 2000-12-18
PRIOR PELING DATE: 2000-12-18
PRIOR PELING DATE: 1999-12-17
PRIOR FILING DATE: 1999-12-17
PRIOR FILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 638
SOFTWARE: PARENTIN OF: 2.1
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Pred. No. 1.2e+06;
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ADDRESSEE: Saliwanchik, iloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.7%; Scorc
100.0%; Pred. No. 1.-...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Feitelson, Jerald S.
Schnepf, H. Ernest
Narva, Kenneth E.
Stockhoff, Brian A.
Schmeits, James
                                                                                                                                        Application US/10022066
o. US20030166057A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 67, Application US/09850351A
Patent No. US20020100080A1
GENERAL INFORMATION:
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ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 4; Conservat
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SSLF
                                                                                                                  10-022-066-231
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US-09-850-351A-67
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OTHER INFORMATION: Xaa represents any amino acid at this position
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ORGANISM: Artificial Sequence
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                                                                                                                      Conservative
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Best Local Similarity
Matches 4; Conserv
                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
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            ; OTHER INFORMUS-10-032-950-3
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APPLICANT: Mayville, Patricia
APPLICANT: Mayville, Patricia
APPLICANT: No. US20020074453Alick, Richard P.
APPLICANT: Beavis, Ronald
APPLICANT: Ji, Guangyong
TITLE OF INVENTION: NOVEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: INTERFERENCE
FILE REFERENCE: 600-1-231N
CURRENT FILING NATE: 1990-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
NUVBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide OTHER INFORMATION: PEDTIDE OTHER INFORMATION: (5) OTHER INFORMATION: (5) OTHER INFORMATION: Xaa represents any amino acid at this position.
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ORGANIZAM: Artificial Sequence
ORGANIZAM: Artificial Sequence: Synthetic
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Deptide
LOCATICN: (5)
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APPLICANT: May111e, Patricia
APPLICANT: May111e, Patricia
APPLICANT: May111e, Patricia
APPLICANT: Beavis, Ronald
APPLICANT: Beavis, Ronald
APPLICANT: Beavis, Ronald
APPLICANT: 11, Guangyong
TITLE OF INVENTION: INTERFERENCE
TITLE OF INVENTION: INTERFERENCE
TITLE OF INVENTION: UNTERFERENCE
CURRENT APPLICATION UNYBER: US/10/032,950
CURRENT FILING DATE: 2001-12-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.7%; Score 18; DB 13; Length 9; 100.0%; Pred. No. 1.2e+06; ive 0; Mismatches 0; Indels
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PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/10032950 Publication No. US20020077453A1 GENERAL INFORMATION:
                                                                                                                                                                  Sequence 2, Application US/10032950 Publication No. US20020077453A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 4; Conservative
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                                                   6 SSLF 9
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Sequence 3. Application US/2030078378A1

Publication No. US2030078378A1

GENERAL INFORMATION:
APPLICANT: New York University Medical Center
TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
FILE REFERENCE: 63753/7

CURRENT APPLICATION NUMBER: US/10/201,444

CURRENT PILING DATE: 2002-07-23

PRIOR APPLICATION NUMBER: US/08/861,476

PRIOR PILING DATE: 1997-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                      Gaps
                                                                                                                                                                                                                                                                                    Sequence 4, Application US/10032950;
Publication No. US20020077453A1
GENERAL INFORMATION:
APPLICANT: Muir, Tom
APPLICANT: Mo. US20020077453A1
APPLICANT: No. US20020077453A1ick, Richard P.
TITLE OF INVENTION: NOWEL STAPHYLOCOCCUS PEPTIDES FOR BACTERIAL
TITLE OF INVENTION: 1NTEFFERENCE
FILE REPERENCE: 600-1-227
CURRENT APPLICATION NUMBER: 607090,402
FRIOR PLLING DATE: 1998-06-24
SOFTWARE: PALCATION NUMBER: 607090,402
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PALCATION VOY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: Xaa represents any amino acid at this position US-10-032-950-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
LOCATION: (5)
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                  Length 9;
                     Score 18; DB 13; I
Pred. No. 1.2e+06;
O; Mismatches 0;
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94.7%; Scc...
100.0%; Pre/
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ORGANISM: Staphylococcus aureus
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SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 9
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RESULT 11
US-10-097-175-86
iS-10-097-175-86
iSequence 86, Application US/10097175
iPublication No. US20030045680A1
iGENERAL INFORMATION:
APPLICANT: USCAL, JOHN L.
APPLICANT: OZA, VIBHA B.
APPLICANT: OZA, VIBHA B.
APPLICANT: PINDEIS, MARK A.
ITILE OF INVENTION: PEPTIDIC MODULATORS OF THE ANDROGEN RECEPTOR
ILLE REFERENCE: PPI-110
CURRENT APPLICATION NUMBER: US/10/097,175
CURRENT FILING DATE: 2001-03-12
PRIOR PILING DATE: 2001-03-12
PRIOR PILING DATE: 2001-03-12
PRIOR PILING DATE: 2001-01-18
NUMBER OF ESD ID NOS: 102
NUMBER OF ESD ID NOS: 102
SEQ ID NO 86
LENGTH: 11
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ITILE OF INVENTION: Cellular Kinase Targets and Inhibitors,
ITILE OF INVENTION: Cellular Kinase Targets and Inhibitors,
ITILE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 50036/048002;
CURRENT FILING DATE: 2003-03-25
PRIOR PRICATION NUMBER: US 60/337,990
PRIOR PILING DATE: 2001-11.13
NUMBER OF SEQ ID NOS: 144
SOFTHARE: PastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 94.7%; Score 18; DB 14; Length 11; Best Local Similarity 100.0%; Pred. No. 3.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
; OTHER INFORMATION: Androgen Receptor Binding Polypeptides
US-10-097-175-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , OTHER INFORMATION: Phosphorylation consensus sequence
US-10-293-086-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 12, Application US/10293086; Publication No. US20030134310A1; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 4; Conserv
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UNESULO 29

UNESULO 29

Sequence 266, Application US/10022066

PUBlication No. US20030166057A1

GENERAL INFORMATION:

APPLICANT: HILDERRAND, WILLIAM H.

APPLICANT: PRILLIMAN, KILEY RAE

TITLE OF INVENTION: WETHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND

TITLE OF INVENTION: WETHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND

TITLE OF INVENTION: WETHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND

TITLE OF INVENTION: WINDER: 00/256,410

PRIOR FILING DATE: 2002-09-09

PRIOR FILING DATE: 2000-12-18

PRIOR FILING DATE: 2000-12-18

PRIOR FILING DATE: 2000-12-18

PRIOR FILING DATE: 2000-12-18

PRIOR FILING DATE: 2001-12-18

PRIOR PRIOR DATE: 2001-12-18

PRIOR FILING DATE: 2001-12-18

PRIOR PRIOR DATE: 2001-12-18

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ORGANISM: Arabidopsis Thaliana
OTHER INFORMATION: Sequence located in Unknown at 10-19 and may interact with US-09-572-270A-470
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US-10-022-066-266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 94.7%; Score 18; DB 10; Length 10; Best Local Similarity 100.0%; Pred. No. 3e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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                                       0; Indels
100.0%; Pred. No. 1.2e+06;
tive 0; Mismatches 0;
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ORGANISM: Artificial Sequence
   Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                    6 SSLF 9
                                                                                                     2 SSLF 5
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Gaps

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RESULT 13 US-10-435-666-1

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Gaps

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2 SSLF 5

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APPLICANT: SAI, Wenyaan
APPLICANT: Anderson Maxwell H.
APPLICANT: Anderson Maxwell H.
TITE OF INVENTION: ANTH-MCROBIAL TARGETING CHIMERIC PHARMACEUTICAL
FILE REFRENCE: 2101363-99160,
CURRENT FILING DATE: 2003-06-16
CURRENT FILING DATE: 2002-06-16
PRIOR PLING DATE: 2002-02-14
PRIOR PLING DATE: 2002-02-14
PRIOR PLING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 09/910,358
PRIOR APPLICATION NUMBER: US 09/910,358
PRIOR APPLICATION NUMBER: US 09/910,358
PRIOR PLING DATE: 2001-07-19
PRIOR PLING DATE: 2001-07-19
SOFTWARE: PACENTIN NUMBER: US 09/378,577
PRIOR PLING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 71
SEQ ID NO 43
LENGTH: 12
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Pred. No. 3.6e+02;
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100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MISC_PEATURE

LOCATION: (1)...(12)

COTHER INFORMATION: Xaa is any amino acid

MS-10-706-391-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: October 26, 2004, 16:10:14 Job time : 17.5 secs
               WASHINGTON DENTAL SERVICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Peptide library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                      sckert, Randal
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Sequence 1, Application US/10435666
Publication No. US20040006001A1
GENERAL INFORMATION:
FULL APPLICANT: CARTER, Daniel C.
TITLE OF INVENTION: FERRITIN FUSION PROTEINS FOR USE IN VACCINES AND OTHER APPLICATION TERREST FOR CARNOR 105/40000/DAS.
CURRENT APPLICATION NUMBER: US/10/435,666
CURRENT FILING DATE: 2003-05-12
PRIOR FILING DATE: 2002-05-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 12
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APPLICANT: WASHINGTON DENTAL SERVICE
APPLICANT: Eckert, Randal
APPLICANT: Eckert, Randal
APPLICANT: Oi, Fengxia
APPLICANT: Shi, Wenyuan
APPLICANT: Shi, Wenyuan
APPLICANT: Anderson, Maxwell H.
TITLE OF INVENTION: ANTI-MICROBIAL TARGETING CHIMERIC PHARMACEUTICAL
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: US 09/910,358
PRIOR PLICATION NUMBER: US 09/910,358
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 1209-08-20
NUMBER OF SEQ ID NOS: 71
SEQ ID NO 42
LENGTH: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.7%; Score 18; DB 16;
100.0%; Pred. No. 3.6e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                    94.7%; bcc.
100.0%; Pred. No. ...
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Publication No. US20040137482A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Peptide library US-10-706-391-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 43, Application US/10706391; Publication No. US20040137482A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                     tYPE: PRT CAGANISM: Homo sapiens US-10-435-666-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 SSLF 5
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US-10-706-391-43
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October 26, 2004, 15:46:55; Search time 4.85294 Seconds (without alignments) 99.132 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                              283416 segs, 96216763 residues
                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                            BLCSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                        US-10-032-950-8
19
1 XSSLF 5
                                                                                                                                                                        Title:
Perfect score:
Sequence:
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                                                                                                     Run on:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

283416

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Description	.0	tropin - c	8	g hear	Ig heavy chain V r				AgrD protein [impo	•	hypothetical prote	hypothetical prote	$^{\circ}$	hypothetical prote		glutelin II 7.4/32	_	hypothetical prote	_	_	ical	plasmid stabilizat	exodeoxyribonuclea	hypothetical prote	protein F17L21.12	Ħ	hypothetical prote	ť.	hypothetical prote
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Query	March	4.	4,	4.	94.7	94.7	94.7	94.7	94.7	94.7	94.7	94.7	94.7		94.7		94.7		94.7		4	4		94.7						94.7
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hypothetical prote hypothetical prote hypothetical prote		hypothetical prote hypothetical prote hypothetical prote	probable phage-rel hypothetical prote conserved hypothet	ZK112.4 protein - probable lipoprote very hypothetical hypothetical prote	
S19984 S19987 C69013	C84274 AB2604 C82369	QQECXP G64521 C71984	AG0277 A83971 F98105	\$44892 \$73700 T38892 G71025	
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888	8 8 8 8 4 3	9 9 9 9 9 9 9 9	95 99 99	100 101 101	
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18 18 18	18 18 18	18 18	18 18	1 1 1 1 1 1 8 8 1 1 1 1 1 1 1 1 1 1 1 1	
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ALIGNMENTS

RESULT 1
 S57518 Total Account of April 17 region , himan (fragment)
C.Species: Homo sabiets (man)
C;Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
 C. C. Accession: S-7-118 R:Burrows, S.R.: Silins, S.L.: Moss, D.J.: Khanna, R.: Misko, I.S.; Argaet, V.P.
 A,Description: T cell receptor repertoire for a viral epitope in humans is diversified in a Reference number: 857494
Arcesion: S57518
A, Status: preliminary
A FKOLECULE LYPE: MKNA A:Residues: 1-18 <bur></bur>
 A,Cross-references: EMBL:Z49920; NID:g887490; PIDN:CAA90166.1; PID:g887491
 C;Keywords: T-cell receptor
94.7%; Score 18; DB 2; Length 18; larity 100.0%; Pred. No. 66;
vative 0; Mismatcl
 Cy 2 SSLF 5
 Db 3 SSLF 6
BESTILT.
 somatotropin - guinea pig (fragment) N.altarnata names - growth hormone
 a pig)
C;Date: 28-April993 #sequence_revision:28-Apr-1993 #text_change 1/-mar-1999 C:bate:28-April993 #sequence_revision:28-Apr-1993 #text_change 1/-mar-1999
R. Gabrielson, B.; Fairhall, K.M.; Robinson, I.C.A.F.
J. Endocrinol. 124, 371-380, 1990
 A,Title: Growth hormone secretion in the guinea-Pig. A,Reference number: A60739; MUID:90237710; PMID:1970601
A;Accession: A60739
A Molecule type: protein
C; Comment: The growth hormone system in the guinea pig is unusual among mammals in that
C;Superramily: prolactin C;Keywords: anterior pituitary; growth factor; hormone
 Score 18;
 Best Local Similarity 100.0%; Pred. No. 74; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 2 SSLF 5
 C. (1) C. (1)
 / SSLF

Gaps

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Windcarburn, L.R.; O'Hehir, R.E.; Hewitt, C.R.; Lamb, J.R.; Owen, M.J.

Froc. Natl. Acad. Sci. U.S.A. 90, 8214-8218, 1993
A;Title: In vivo clonal dominance and limited T-cell receptor usage in human CD4+ T-cell
A;Reference number: A47719; MUD:93376774; PMID:8367485
A;Accession: E47719
A;Accession: E47719
A;Accession: E47719
A;Accession: Columnary
A;Accession: Colum
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C;Species: chloroplast Picea abies (Norway spruce)
C;Date: 16-Uul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T11814
R;Kluemper, S.; Kanka, S.; Riesner, D.; Etscheid, M.
submitted to the EMBL Data Library, March 1997
A;Description: Characterisation of a Norway spruce chloroplast DNA clone: Complete nucle
A;Reference number: 217349
A;Accession: T11814
A;Accession: T11814
A;Accession: J1344
A;Accession: J1344
A;Residues: 1-34 <KLU;
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hypochetical protein ECs1538 [imported] - Escherichia coli (strain O157:H7, substrain RI
C;Date: Bscherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: B90821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           house-dust-mite-reactive T-cell receptor beta chain (CD4+ clone DE26, V(D)J junctional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C;Accession: E47719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:062958; EMBL:U92462; NID:g2959581; PID:g2959590 C;Genetics:
C, Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                          24;
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                    0; Indels
                                                                                                                                94.7%; Score 18; DB: 100.0%; Pred. No. 89; ive 0; Mismatches
                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 100.
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C; Keywords: chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                           19 SSLF 22
                                                                                                                                                                                                                                                                                                                          2 SSLF 5
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                                                                                                                  Total receptor alpha chain J region (TA20) - mouse (fragment)
CySpecies: Mus musculus (house mouse)
CySpecies: Mus musculus (house mouse)
CyAccession: 503481
RyArden, B.; Klotz, J.L.; Siu, G.; Hood, L.E.
Nature 316, 783-787, 1885
A;Title: Diversity and structure of genes of the alpha family of mouse T-cell antigen re A;Reference number: 803467; MUID:85296324; PMID:3839904
A;Accession: 803481
A;Residues: 1-21 cARD>
A;Residues: 1-21 cARD>
A;Coss-references: EMBL:X02975; NID:954392; PIDN:CAA26717.1; PID:9773240
A;Note: this sequence was determined from the differentiated gene
C;Keywords: T-cell receptor alpha chain J region #status predicted cJRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
PH1697
Igh heavy chain V region - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C.Accession: PH1697; HR1699
R.MCHEYZER Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
A.Filtle: Antigen-driven B cell differentiation in vivo.
A.Reference number: PH1675; MulD:93301607; PMID:8315385
A.Accession: PH1697
A.Filtle: Antigen-driven B cell; clone NP-7-10
A.Fixperimental source: B cell; clone NP-7-10
A.Fixperimental source: B cell; clone NP-7-12
A.Ficession: PH1699
A.MOlecule type: mRNA
A.Residues: 1-24 cMCH>
A.Fixperimental source: B cell; clone NP-7-12
C.Superimental source: B cell; clone NP-7-12
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PHIG96
PHIG96
IG heavy chain V region (clone NP-7-9) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C;Accession: PHIG94
A;McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
A;Title: Antigen-driven B cell differentiation in vivo.
A;Reference number: PHIG75; MUID:93301607; PMID:8315385
A;Accession: PHIG96.
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A, Molecule type: mRNA A, Residues: 1-24 <MCH> A, Experimental source: B cell

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Approximation procession: yearden pea)
(c)Species: Bium sativum (garden pea)
(c)Species: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
(c)Accession: T06514
(c)Accession: T06514
(c)Accession: T06514
(c)Accession: Data Library, June 1996
(c)Accession: Pea S-adenosylmethionine decarboxylase.
(a)Accession: T06514
(c)Accession: T06514
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C,Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 03-Jun-2002
C,Accession: S01877
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C'Species: Rickettsia prowazekii
C'Species: Rickettsia prowazekii
C'Species: Rickettsia prowazekii
C'Species: Rickettsia prowazekii
C'Date: 21.Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C'Accession: B71683
RAndersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Natule: 396, 133-140, 1998
AyAndersson, S.G.E.; Anterest of Rickettsia prowazekii and the origin of mitochondria. A; Reference number: A71630; MUID:99039499; PMID:9823893
A; Accession: B71683
A; Accession: B71683
A; Reference number: DNA
A; Residues: 1-55 AND
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       A,Pathway: nucleotide biosynthesis
C,Superfamily: ribose-phosphate pyrophosphokinase catalytic chain
C;Keywords: diphosphotransferase; magnesium; nucleotide biosynthesis
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94.7%; Score 18; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 2e+02;
iive 0; Mismatches (
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C;Genetics:
A;Gene: agrD
                                                                                                                                                                                                                                                                                                                                              A,Cross-references: UNIPROT;Q8X3H3; GB:BA000007; PIDN:BAB34961.1; PID:g13361002; GSPDB:q
A,Experimental source: strain Ol57:H7, substrain RIMD 0509952
C;Genetics:
A,Gene: EC$1538
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C;Species: Listeria ivanovii
C;Date: 02-Dec-1993 #sequence_revision 25-Oct-1996 #text_change 09-Jul-2004
C;Accession: 834405; 834728
R;Lampidis, R.; Gross, R.; Sokolovic, Z.; Goebel, W.; Kreft, J.
Mol. Microbiol. 13, 141-151, 1994
A;Pitle: The virulence regulator protein of Listeria ivanovii is highly homologous to E A;Pitle: The virulence regulator protein of Listeria ivanovii is highly homologous to E A;Reference number: 854403; MUID:95075291; PMID:7984088
A;Accession: 854405
A;Reference caid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-54 cLAM>
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C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: C89995
C;Accession: C89995
C;Accession: C89995
C;Accession: C89995
C;Shiba, T; Uchiyama, I; Baba, T; Yuzawa, H; Kobayashi, I; Cui, L; Ci, Shiba, T; Hattori, M; Ogasawara, N; Hayashi, H; Kobayashi, I; Sekimizu, C; Shiba, T; Hattori, M; Ogasawara, N; Hayashi, H; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Reference number: A89758; MulD:21311952; PMID:11418146
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, Ogasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli Ol57:H7 and gA; Reference number: A99629; MUID:21156231; PMID:11258796
A; Accession: B90821
A; Status: preliminary
A; Residues: DNA
A; Residues: 1-46 cHAY>
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100.0%; Pred. No. 1.7e+02;
ive 0; Mismatches 0;
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A; Molecule type: DNA
A; Residues: 1-47 < KUR>
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A;Gene: prs
C;Function:
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H72168
A43P protein - variola minor virus (strain Garcia-1966)
C;Species: variola minor virus
C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999.#text_change 09-Jul-2004
C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999.#text_change 09-Jul-2004
C;Accession: H72168
R;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar submitted to Ganbank, March 1998
A;Bescription: Analysis of the complete coding sequence of DNA of alastrim variola minor A;Reference number: A72150
A;Accession: H72168
A;Accession: H72168
A;Kesiques: DNA
A;Resiques: 1-62 <SHC>
A;Resiques: 1-62 <SHC>
A;Resiques: 1-62 <SHC>
A;Access-references: UNPROT;Q89183; GB:Y16780; NID:G5830555; PIDN:CAB54746.1; PID:e15427
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C;Genetics:
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T07470
hypothetical protein 62b - Japanese black pine chloroplast
C;Species: chloroplast Pinus thumbergiana (Japanese black pine)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C;Accession: T07470
R;Wakasugi, T:; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiura, M.
R;Wakasugi, T:; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiura, M.
R;Wakasugi, T:; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiura, M.
R;Wakasugi, T:; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiura, M.
A;Reference number: Z16030; MulD:95024047; PMID:7937893
A;Accession: T07470
A;Accession: T07470
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-62 -WAKA
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R;Batuecas, B.; Garesse, R.; Calleja, M.; Valverde, J.R.; Marco, R. Nucleic Acids Res. 16, 6515-6529, 1988
A;Title: Genome organization of Artemia mitochondrial DNA.
A;Reference number: S01207; MUID:88289417; PMID:3135541
A;Rocession: S01877
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94.7%; Score 18; DB 2; Lv
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
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C,Keywords: chloroplast
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Name=RAGE;
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127.445 Million cell updates/sec
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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ALIGNMENTS

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RESULT 3 Q9Z068 ID Q9Z06

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27 27
27 AA; 2716 MW; C0F6555B3CF5925A CRC64;
                                                              94.7%; Scor.
100.0%; Pred. No. >...
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0; Mismatches
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                                                                                                                                                                                                                                                                                           Envelope protein (Fragment)
                                                                                                    4; Conservative
                                                                                                                                                                                                                          PRELIMINARY;
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                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
    Envelope protein.
NON_TER 1
NON_TER 27
SEQUENCE 27 AA;
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Best Local Similarity
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01-JUN-2003
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Q9J5X4;
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Polyprotein; Transmembrane.
NON TER
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
E2 region (Fragment).
Heparitis C virus.
Viruses; SSRNA positive-strand viruses, no DNA stage; Flaviviridae;
NCBL_TAXID=11103;
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Hepacivirus.
NCBI_TaxID=11103;
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Mizuno M., Hayuchi T., Kanmarsuse K., Esumi M.;
"Genetic and serological evidence for multiple instances of
unrecognized transmission of hepatitis C virus in hemodialysis
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                                                    94.7%; Score 18; DB 2; Length 27; 100.0%; Pred. No. 9.6e+02; ive 0; Mismatches 0; Indels
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF221141; AAF77703.1; -.
GO; GO:0019031; C;viral envelope; IEA.
                           27 AA; 2769 MW; 707B66F95EC388D4 CRC64;
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EMBL; AB001404; BAA35043.1; -

EMBC; AB0011404; Cintegral to membrane; IEA.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0019918; F:structural molecule activity; IEA.

InterPro; IPR002531; HCV_NS1.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Envelope protein (Fragment)
                                                                                                                                                                                                          27 AA.
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                                                     Query Match
Best Local Similarity 100.
Matches 4; Conservative
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Hydrolase, Protease,
NON TER 27
SEQUENCE 27 AA; 2
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Matches

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Alberto S.-F.,

Alberto S.-F.,

Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

BRBL, AF21140; AAF7702.1; -

CR GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0019028; C:viral capsid; IEA.

R GO; GO:0019028; C:viral envelope; IEA.

R GO; GO:0019018; F:structural molecule activity; IEA.

R GO; GO:005198; F:structural molecule activity; IEA.
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Manzin A., Solforosi L., Debiaggi M., Zara F., Tanzi B., Romano L.,
Manzin A.R., Clementi M., Debiaggi M., Zara F., Tanzi B., Romano L.,
"Dominant role of host selective pressure in driving hepatitis C virus
evolution in perinatal infection.";
J. Virol. 74:4227-4334(2000).
EMBL; AF192435; AAF65646.1;
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Hepacivirus.
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Hepacivirus,
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Score 18; DB 2; Length 27;
Pred. No. 9.6e+02;
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Pred. No. 9.6e+02;
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(TrEWBLrel. 15, Last sequence update)
(TrEWBLrel. 24, Last annotation update)
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27 AA.

Length 27;

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SEQUENCE FROM N.A.
MEDLINE=20219428; PubMed=10756048;
Manzin A., Solforosi L., Debiaggi M., Zara F., Tanzi E., Romano L.,
Zanetti A.R., Clementi M.;
"Dominant role of host selective pressure in driving hepatitis C virus
evolution in perinaral infection.";
J. Virol. 74:4327-4334(2000).
EMBL; AF192429; AAF65640.1; -.
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=20219428; PubMed=10756048;
MEDLINE=20219428; PubMed=10756048;
Manzin A. Solfcosi L., Debiaggi M., Zara F., Tanzi E., Romano L.,
Zanctti A.R., Clementi M.;
"Dominant role of host selective pressure in driving hepatitis C virus
evolution in perinatal infection.";
J. Virol. 74:4227-4334 (2000).

EMBL; AF192430; AAF65641.1;
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Hepatitis C virus.
Viruses, SRNA positive-strand viruses, no DNA stage; Flaviviridae;
NCBI_TaxID=11103;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Polyprotein (Fragment)
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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94.7%; Score 18; DB 2; Length 27;

Best Local Similarity 100.0%; Pred. No. 9.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels
                      94.7%; Score 18; DB 2; Length 27; 100.0%; Pred. No. 9.6e+02; ive 0; Mismatches 0; Indels
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2C72839C79B20A04 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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2825 MW;
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MEDLINE=20219428; PubMed=10756048;
Manzin A., Solforosi I., Debiaggi M., Zara F., Tanzi E., Romano L.,
Zanetri A.R., Clementi M.;
"Dominant zole of host selective pressure in driving hepatitis C virus
evolution in perinatal infection.";
J. Virol. 74:4327-4334(2000)
EMBL; AF192432; AAF65643.1; -.
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SEQÜENCE 27 AA; 2842 MW; 2C72814C79B20A04 CRC64;
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MEDLINE=20219428; PubMed=10756048;
MEDLINE=20219428; PubMed=10756048;
Manzin A., R., Olementi M.;
Zanetti A.R., Olementi M.;
"Dominant role of host selective pressure in driving hepatitis C virus evolution in perinatal infection.";
J. Virol. 74:4327-4334(2000).
EMBL; AF192431; AAF65642.1; -.
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01-OCT-2000 (TEMBLrel. 15, Last sequence update)
01-OCT-2002 (TEMBLrel. 15, Last annotation update)
01-OCT-2002 (TEMBLrel. 22, Last annotation update)
Polyprotein (Fragment).
Hepatitis C virus.
Viruses; SSRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                     Q9JSX7;
Q1-COT-2000 (TrEMBLrel. 15, Created)
O1-COT-2000 (TrEMBLrel. 15, Last sequence update)
O1-CCT-2002 (TrEMBLrel. 22, Last annotation update)
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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94.7%; Score 18; DB 2; Length 27;

Best Local Similarity 100.0%; Pred. No. 9.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels
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27 AA; 2839 MW; 2C7284EC79B20A04 CRC64;
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Score 18; DB 2;
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01-UNV-2002 (TrEMBLrel. 21, C:
01-UNV-2002 (TrEMBLrel. 21, Le
01-UNV-2003 (TrEMBLrel. 24, Le
E2 protein (Fragment).
Hepatitis C virus.
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J. Virol. 74:4327-4334(2000).

EMBL; AF192424; AAF65635.1;
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Hepacivirus.
NCBI_TaxID=11103;
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   100.0%; Pred. No. 9.6e+02;
tive 0; Mismatches 0; Indels
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27 AA; 2852 MW; 08B36BEC79B20A1E CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Polyprotein (Fragment).
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Polyprotein (Fragment).
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Best Local Similarity 100.
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MEDINE=22786443; PubMed=12904364;

MEDINE=20101011; Medine=20101 Sequences to predict antiviral outcome.";

MEDINE=22786443; PubMed=129043; PubMed=12623;

MEDINE=227864473776; Abla86846.1; PubMed=1263;

MEDINE=2276641, PubMed=1263;

MEDINE=2276474776; Abla86846.1; PubMed=1263;

MEDINE=227684447776; Medine=22764;

MEDINE=2276844477304D5 CRC64;

MEDINE=2276844477304D5 CRC64;

MEDINE=22764744477304D5 CRC64;
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MEDLINE=20219428; PubMed=10756048;
Manzin A., Solforosi L., Debiaggi M., Zara F., Tanzi E., Romano L.,
Zanetti A.R., Clementi M.;
"Dominant role of host selective pressure in driving hepatitis C virus
evolution in perinatal infection.";
J. Virol. 74:427-4334(2000).
EMBL; AF192423; AAF65634.1; -.
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                                        01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Polyprotein (Fragment).
Hepatitis C virus.
Viruses; seRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Hepacivirus.
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01-JUN-2002 (TEMBLrel. 21, Created)
01-JUN-2003 (TEMBLrel. 21, Last sequence update)
01-JUN-2003 (TEMBLrel. 24, Last annotation update)
E2 protein (Fragment).
Hepatitis C virus.
Hepatitis C virus.
Hepatitis C virus.
Norinses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
NCBI_TAXID=11103;
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94.7%; Score 18; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
Best Local Similarity 100.0%; Pred. No. 9.6e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 27
27 AA; 2674 MW; A7F417F44073C4D5 CRC64;
                                                                                                                                27 AA.
                                                                                                                                PRELIMINARY;
                                                               17 SSLF 20
                                       2 SSLF 5
                                                                                                      RESULT 15
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17 SSLF 20

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